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Tami M Procopio

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In the application of:

Aya Jakobovits, et al.

Serial No.: 10/001,469

Filing Date: October 31, 2001

For: NUCLEIC ACID AND CORRESPONDING PROTEINS ENTITLED 101P3A11 USEFUL IN TREATMENT AND DETECTION OF CANCER

Examiner: To be Assigned

Group Art Unit: 1642

AMENDMENT

Box Missing Parts
Assistant Commissioner For Patents
Washington, D.C. 20231

Dear Sir:

This is in response to the Notice to file missing parts of non-provisional application mailed December 20, 2001, for which a response is due on February 20, 2002. A petition for an extension of time of three (3) months until 20 May 2002 is attached hereto, along with the required fee.

Please enter the following sequence listing, amendments and remarks.

sd-79244

In the Specification

On page 1, line 26, please insert new paragraph as follows:

--SUBMISSION ON COMPACT DISC

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: A compact disc copy of the Sequence Listing (COPY 1) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB); a duplicate compact disc copy of Sequence Listing (COPY 2) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB); a computer readable form copy of the Sequence Listing (CRF COPY) (file name: 2002420, date recorded: February 16, 2002, size: 569 KB).--

In the Sequence Listing

Please insert the attached compact disc copy of the Sequence Listing on CD-R (COPY 1) in the above-captioned application. A duplicate compact disc copy of the Sequence Listing on CD-R (COPY 2) and a computer readable form copy of the Sequence Listing on CD-R (CRF COPY) accompany this response.

AMENDMENTS

In the Specification:

Please replace the paragraph beginning at page 7, line 21, with the following rewritten paragraph:

-- **Figure 1. 101P3A11 SSH sequence (SEQ ID NO:2960).** The 101P3A11 SSH sequence.--

Please replace the paragraph beginning at page 7, line 22, with the following rewritten paragraph:

-- **Figures 2A-2D. The cDNA (SEQ ID. NO. :2961) and amino acid sequence (SEQ ID. NO. :2962) of 101P3A11.** The start methionine is underlined. The open reading frame extends from nucleic acid 133 to 1086 including the stop codon (the codon for the initial M is omitted as the shorter peptide has a more favorable Kozak sequence).--

Please replace the paragraph beginning at page 7, line 26, with the following rewritten paragraph:

--**Figure 3. Amino acid sequence of 101P3A11 (SEQ ID. NO. :piece of 2962).** The 101P3A11 protein has 317 amino acids.--

Please replace the paragraph beginning at page 7, line 28, with the following rewritten paragraph:

--**Figure 4. Alignment of 101P3A11 (Sbjct) (SEQ ID NO: 2964) with mouse olfactory receptor S25 (Query.) (SEQ ID NO: 2963)** The transmembrane regions of 101P3A11 and mouse olfactory receptor S25 (ORS25)predicted using the TMHMM algorithm are highlighted in gray. The amino acids of ORS25 predicted (Floriano, W.B., et al, 2000, Proc. Natl. Acad. Sci., USA, 97:10712-10716) to be involved in binding of the ligand hexanol and/or involved in the formation of the ligand binding pocket are italicized and bolded in the Figure, and are: Leu 131, Val 134, Val 135, Gly 138, Thr139, Ser 193, Ser 197, Phe 225, Ala 230, Ile 231, Gly 234, Thr 284, Phe 287, Gln 300, Lys 302.--

Please replace the paragraph beginning at page 11, line 31, with the following rewritten paragraph:

--**Figure 23.** Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2965) with the rat (SEQ ID NO: 2966) GPCR RA1C (gi|3420759). Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%).--

Please replace the paragraph beginning at page 12, line 1, with the following rewritten paragraph:

--**Figure 24.** Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2967) with the human prostate specific GPCR (SEQ ID NO: 2968) (gi|13540539). Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%).--

Please replace the paragraph beginning at page 12, line 3, with the following rewritten paragraph:

--**Figure 25.** Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2969) with human olfactory receptor 5lI12, HOR5 (SEQ ID NO: 2970) (gi|14423836). Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%).--

Please replace the paragraph beginning at page 36, line 20, with the following rewritten paragraph:

--Also, different MHC class I molecules prefer a different length of ligands. For example, SYFPEITHI offers predictions for H2-Kb octamers, HLA-A*0201 nonamers and decamers, or HLA-B8 octamers and nonamers. The maximal scores vary between different MHC alleles. Therefore, one can include known ligands/epitopes in order to have an approximation of the scoring. For example, the maximal score for HLA-A*0201 peptides is 36. The well-known epitope GILGFVFTL (SEQ ID NO: 1401) derived from the influenza A matrix protein scores 30. All predicted MHC class II ligands are 15mers, consisting of three N-terminal flanking residues, the nonamer core sequence located within the binding groove, and three C-terminal flanking residues. Thus, anchor residue P1 appears in position 4 of the peptides predicted with "SYFPEITHI".--

Please replace the paragraph beginning at page 37, line 25, with the following rewritten paragraph:

--In an embodiment described in the examples that follow, 101P3A11 can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 101P3A11 with a C-terminal 6XHis (SEQ ID NO: 1402) and MYC tag (pcDNA3.1/mycHIS, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 101P3A11 protein in transfected cells. The secreted HIS-tagged 101P3A11 in the culture media can be purified, e.g., using a nickel column using standard techniques.--

Please replace the paragraph beginning at page 70, line 3, with the following rewritten paragraph:

--In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; (SEQ ID NO: 1403), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; (SEQ ID NO: 1404), and *Streptococcus* 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; (SEQ ID NO: 1405). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.--

Please replace the paragraph beginning at page 70, line 11, with the following rewritten paragraph:

--Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-

binding epitope peptide having the formula: aKXVAAWTLKAAa (SEQ ID NO: 1406), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.--

Please replace the paragraph beginning at page 80, line 16, with the following rewritten paragraph:

--Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant polynucleotide vectors encoding such single chain antibodies in order to precisely target the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL (SEQ ID NO: 1407) amino acid motif. Intrabodies intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.--

Please replace the paragraph beginning at page 86, line 29, with the following rewritten paragraph:

--pGEX Constructs: To generate recombinant 101P3A11 proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 101P3A11 cDNA protein coding sequence are fused to the GST gene by cloning into pGEX-6P-1 or any other GST- fusion vector of the pGEX family (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) (SEQ ID NO: 1402) at the carboxyl-

terminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag (SEQ ID NO: 1402) is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScission™ recognition site in pGEX-6P-1, can be employed that permits cleavage of the GST tag from 101P3A11-related protein. The ampicillin resistance gene and pBR322 origin permit selection and maintenance of the pGEX plasmids in *E. coli*. In one embodiment, amino acids 86-317 are cloned into the pGEX-2T expression vector, the protein is expressed and purified.--

Please replace the paragraph beginning at page 87, line 8, with the following rewritten paragraph:

--pMAL Constructs: To generate, in bacteria, recombinant 101P3A11 proteins that are fused to maltose-binding protein (MBP), all or parts of the 101P3A11 cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors (New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with MBP fused at the amino-terminus and a 6X His (SEQ ID NO: 1402) epitope tag at the carboxyl-terminus. The MBP and 6X His tags (SEQ ID NO: 1402) permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His (SEQ ID NO: 1402) epitope tag is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 101P3A11. The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds. In one embodiment, amino acids 86-310 is cloned into the pMAL-c2X expression vector, the protein is expressed and purified.--

Please replace the paragraph beginning at page 87, line 20, with the following rewritten paragraph:

--pET Constructs: To express 101P3A11 in bacterial cells, all or parts of the 101P3A11 cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 101P3A11 protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His (SEQ ID NO: 1402) and S-Tag ™ that aid purification and detection of the recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 101P3A11 protein are expressed as amino-terminal fusions to NusA.--

Please replace the paragraph beginning at page 88, line 19, with the following rewritten paragraph:

--**pcDNA4/HisMax Constructs:** To express 101P3A11 in mammalian cells, the 101P3A11 ORF was cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has Xpress™ and six histidine (6X His) (SEQ ID NO: 1402) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.--

Please replace the paragraph beginning at page 88, line 28, with the following rewritten paragraph:

--**pcDNA3.1/MycHis Constructs:** To express 101P3A11 in mammalian cells, the 101P3A11 ORF, with a consensus Kozak translation initiation site, was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the myc epitope and 6X His (SEQ ID NO: 1402) epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and

simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene can be used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.--

Please replace the paragraph beginning at page 89, line 16, with the following rewritten paragraph:

--**PAPtag:** The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of the 101P3A11 proteins while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of 101P3A11 proteins. The resulting recombinant 101P3A11 proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His (SEQ ID NO: 1402) epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.--

Please replace the paragraph beginning at page 89, line 27, with the following rewritten paragraph:

--**ptag5:** The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pTag-5. This vector is similar to pAPtag but without the alkaline phosphatase fusion. This construct generated 101P3A11 protein with an amino-terminal IgGκ signal sequence and myc and 6X His (SEQ ID NO: 1402) epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 101P3A11 protein was optimized for secretion into the media of transfected mammalian cells, and was used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for

selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.--

Please replace the paragraph beginning at page 90, line 30, with the following rewritten paragraph:

--Additional pSRα constructs are made that fuse an epitope tag such as the FLAG™ tag to the carboxyl-terminus of 101P3A11 sequences to allow detection using anti-Flag antibodies. For example, the FLAG™ sequence 5' gat tac aag gat gac gac gat aag 3' (SEQ ID NO: 1408) is added to cloning primer at the 3' end of the ORF. Additional pSRα constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His (SEQ ID NO: 1402) fusion proteins of the full-length 101P3A11 proteins.--

Please replace the paragraph beginning at page 141, line 31, with the following rewritten paragraph:

--The generation of anti-101P3A11 polyclonal Ab (pAb) using an amino-terminal peptide encoding amino acids 1-14 (MVDPNGNESSATYF; (SEQ ID NO: 1409) as antigen was reported in our Priority Application. The effect of this antibody on 101P3A11 mediated ERK phosphorylation (Figure 38) and cAMP accumulation (Figure 39) was determined. 293T cells were transfected with control or 101P3A11 cDNA. Cells were allowed to rest overnight, and treated with anti-101P3A11 or control Ab in the presence of 0.5% or 10% FBS. Cells were lysed and analyzed by Western blotting with anti-Phospho-ERK and anti-ERK mAb. Figure 38 shows that expression of 101P3A11 induces ERK phosphorylation in cells treated with 0.5 or 10% FBS. Anti-101P3A11 pAb reduced the phosphorylation of ERK in 293T-101P3A11 cells treated with 0.5% FBS. The ERK overlay demonstrated equal loading, supporting the specificity of this data.--

Please replace Table XIX, beginning at page 186, with the following rewritten Table XIX:

--Table XIX: Motifs and Post-translational Modifications of 101P3A11

N-glycosylation site

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Number of matches: 3
1 7-10 NESS (SEQ ID NO: 1410)
2 44-47 NLTI (SEQ ID NO: 1411)
3 90-93 NSTT (SEQ ID NO: 1412)

cAMP- and cGMP-dependent protein kinase phosphorylation site
268-271 RRDS (SEQ ID NO: 1413)

Protein kinase C phosphorylation site
266-268 SKR

Casein kinase II phosphorylation site
Number of matches: 3
1 56-59 SLHE (SEQ ID NO: 1414)
2 69-72 SGID (SEQ ID NO: 1415)
3 110-113 SGME (SEQ ID NO: 1416)

N-myristoylation site
Number of matches: 4
1 6-11 GNESSA (SEQ ID NO: 1417)
2 21-26 GLEEAQ (SEQ ID NO: 1418)
3 111-116 GMESTV (SEQ ID NO: 1419)
4 240-245 GTCVSH (SEQ ID NO: 1420)

G-protein coupled receptors family 1 signature
112-128 MESTVLLAMAFDRYVAI (SEQ ID NO: 1421)--

Please replace Table XXI, beginning at page 190, line 1, with the following rewritten Table XXI:

--**Table XXI: Nucleotide sequence of the splice variant** (SEQ ID NO: 1422)

```
   1 CACATTCCTT CCATACGGTT GAGCCTCTAC CTGCCTGGTG CTGGTCACAG TTCAGCTTCT
  61 TCATGATGGT GGATCCCAAT GGCAATGAAT CCAGTGCTAC ATACTTCATC CTAATAGGCC
 121 TCCCTGGTTT AGAAGAGGCT CAGTTCTGGT TGGCCTCCCA TTGTGCTCCC TCTANCTATG
 181 CTGTGCTAGT AATTGACAAT CATCTACATG TGCGGACGAG CACGNCGCNG AGCCCNGTAT
 241 NATTCTGCNG CTTCAGCATG ACACCCTNCA GTCTCAGCCA AAGNGCATCT CNGTCAATCA
 301 NACACNTGAG CTGTCGTACG AGTTGCATCA TCCTANGGCA GGATCAATGT GCGGNAGGCN
 361 TGACGCAGTG CACGTACCAT GGCAGCAAGA CAGGGCCGGT ACAAATGGGG GCGAGNCGGG
 421 GTGAAGATGN ACCCTCGGGT CANAGAGTGC CTCTGCGCCA AAACCTCCAT CATGNNAACA
 481 GNGTATAACG GCGNAGAATC GGNNANGCGC AAGGCTAAGG AAANNCCCAA NNCNGGTACT
 541 TTAACCCNGC AAANGGCANC NAAACGGGNG GGTNANTGAA CAAGGAAGGN NTGNAACTGG
 601 GCCAAAACGG GNTGGGCAAN NNAAGGACTC ATGGGNCCAA GGGACGGNAA AAGGGGNAAN
 661 CGGGGCGAAA TGNNAAAAAC CGGGNCCCGG GGAANAANGA AGGGGAANAN GNGTGAAGGA
 721 CNGGGTTCAA GGGAAAAGNA AAACCANGGG NNAGAAACCN TTCNAANGGC CCGGGNANGA
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781 AAGGAANTNN GNNNGGNGAA AAAATCNAAA AAAAGCNGNG GCNNAAAAAN GGGGGGAANN
841 NAAANACCNN GGNCGNNAAA AAACNNAANG NGGGGGGANT ANACACGGAA ANNNANGGGC
901 GNNNAAGGGA AATAANNCGG GAACNAAAGN GCAAACCGNA CGGNAGGAAC GAAACCCACC
961 GGAGNCGCNN AACGCCNNNC NNANCCCGAG CNGAGGTNG--
```

Please replace Table XXII, beginning at page 190, line 38, with the following rewritten Table XXII:

--Table XXII: Nucleotide sequence alignment of 101P3A11 with the splice variant.

Score = 337 bits (175), Expect = 4e-89
Identities = 215/223 (96%), Gaps = 6/223 (2%)
Strand = Plus / Plus

```
101P3A11: 68  cacattccttccatacggttgagcctctacctgcctggtgctggtcacagttcagcttct 127
(SEQ ID NO: 1423)
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Variant : 1   cacattccttccatacggttgagcctctacctgcctggtgctggtcacagttcagcttct 60
(SEQ ID NO: 1424)

101P3A11: 128 tcatgatggtggatcccaatggcaatgaatccagtgctacatacttcatcctaataggcc 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Variant : 61  tcatgatggtggatcccaatggcaatgaatccagtgctacatacttcatcctaataggcc 120

101P3A11: 188 tccctggtttagaagaggctcagttctggttggccttcccattgtgctccctctacctta 247
              |||||||||||||||||||||||||||||||||| |||||||||||||||||| ||
Variant : 121 tccctggtttagaagaggctcagttctggttggcc-tcccattgtgctccctctanct-- 177

101P3A11: 248 ttgctgtgctaggtaacttgacaatcatctacattgtgcggac 290
              |||||||||| |||| |||||||||||||||| |||||||||
Variant : 178 atgctgtgcta-gtaa-ttgacaatcatctaca-tgtgcggac 217--
```

Please replace Table XXIII, beginning at page 191, line 8, with the following rewritten Table XXIII:

--Table XXIII: Longest single amino acid sequence alignment of 101P3A11 and the splice variant.

Score = 134 bits (287), Expect(2) = 3e-29
Identities = 51/51 (100%)
Frame = +1 / +3

```
101P3A11: 70  HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 222
(SEQ ID NO: 1425)
              HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA
Variant : 3   HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 155
(SEQ ID NO: 1426)--
```

Please replace Table XXIV, beginning at page 191, line 16, with the following rewritten Table XXIV:

--Table XXIV: Peptide sequences from the translation of the nucleotide sequence of the splice variant .

Open reading frame	Amino acid sequences
Frame 1 (SEQ ID NO: 1427)	HIPSIRLSLYLPGAGHSSASS*WWIPMAMNPVLHTSS**ASLV*KRLSSGWPPIVLPLXM LC**LTIIYMCGRARRXAXYXSAASA*HPXVSAKXHLXQSXT*AVVRVASSXGRINVRXA *RSARTMAARQGRYKWGRXGVKMXPRVXECLCAKTSIMXTXYNGXESXXRKAKEXPXXGT LTXQXAXKRXGX*TRKXXNWAKTGWAXXGLMGPRDGKRGXRGEMXKTGXRGXXKGXXXEG XGSREKXNXGXETXXXARXXKEXXXXKKSKKSXGXKXGGXXXPXXXKNXXXGXXTRKXXG XXGK*XGNXXANRTXGTKPTGXAXRXXXPEXRX
Frame 2(SEQ ID NO: 1428)	TFLPYG*ASTCLVLVTVQLLHDGGSQWQ*IQCYILHPNRPPWFRRGSVLVGLPLCSLXLC CASN*QSSTCADEHXAEPXXILXLQHDTLQSQPKXISVNXTXELSYELHHPXAGSMCGRX DAVHVPWQQDRAGTNGGEXG*RXTLGSXSASAPKPPSXXQXITAXNRXXARLRKXPXXVL *PXKXXXNGXVXEQGRXXTGPKRXGQXKDSWXQGTXKGXXGAKXXKPGPGEXXRGXXVKD XVQGKXKTXGXKPFXXPGXERXXXXXKNXKKAXAXKXGEXKXXGRXKTXXGGXXHGXXXA XKGNXXGTKXQTXRXERNPPEXXNAXXXPSXG
Frame 3(SEQ ID NO: 1429)	HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLASHCAPSXYA VLVIDNHLHVRTSTXXSPVXFCXFSMTPXSLSQXASXSIXHXSCRTSCIILXQDQCAXGX TQCTYHGSKTGPVQMGAXRGEDXPSGXRVPLRQNLHHXNXV*RRRIGXAQG*GXXQXXYF NPAXGXXTGGXXNKEGXXLGQNGXGXXRTHGXKGRXKGXXGRNXKNRXPGXXEGEXX*RT GFKGKXKPXXRNXSXGPGXKGXXXGEKIXKKXXXKXGGXXXTXXXKKXXXGGXXTEXXGR XREIXREXKXKPXGRNETHRXRXTPXXXRAEV

Note: Frame 3 gives the longest subsequence that is identical with 101P3A11 amino acid sequence. In this Table each (*)indicates the product of a single stop codon, and 'X' indicates a single unknown amino acid.--

Please replace Table XXVI, beginning at page 193, line 1, with the following rewritten Table XXVI:

--Table XXVI:
HLA Class I Nonamers (SEQ ID NOS 1430-1462, respectively in order of appearance)

HLA-A1 nonomers

	Pos	1	2	3	4	5	6	7	8	9	score
1	245	H	V	C	A	V	F	I	F	Y	24
2	29	L	A	F	P	L	C	S	L	Y	21
3	41	V	L	G	N	L	T	I	I	Y	21
4	285	P	P	V	L	N	P	I	V	Y	20
5	111	G	M	E	S	T	V	L	L	A	19
6	117	L	L	A	M	A	F	D	R	Y	19
7	172	R	S	N	I	L	S	H	S	Y	19
8	192	D	D	I	R	V	N	V	V	Y	19
9	212	D	S	L	L	I	S	F	S	Y	19
10	57	L	H	E	P	M	Y	I	F	L	18
11	22	L	E	E	A	Q	F	W	L	A	17
12	9	S	S	A	T	Y	F	I	L	I	16
13	52	R	T	E	H	S	L	H	E	P	16

HLA-A1 nonomers

	Pos	1	2	3	4	5	6	7	8	9	score
14	54	E	H	**S**	L	H	E	P	M	**Y**	16
15	78	S	S	**M**	P	K	M	L	A	**I**	16
16	95	Q	F	**D**	A	C	L	L	Q	**I**	16
17	159	A	P	**L**	P	V	F	I	K	**Q**	16
18	183	H	Q	**D**	V	M	K	L	A	**C**	16
19	1	M	V	**D**	P	N	G	N	E	**S**	15
20	5	N	G	**N**	E	S	S	A	T	**Y**	15
21	210	G	L	**D**	S	L	L	I	S	**F**	15
22	273	L	P	**V**	I	L	A	N	I	**Y**	15
23	271	S	P	**L**	P	V	I	L	A	**N**	14
24	91	S	T	**T**	I	Q	F	D	A	**C**	13
25	121	A	F	**D**	R	Y	V	A	I	**C**	13
26	138	L	T	**L**	P	R	V	T	K	**I**	13
27	218	F	S	**Y**	L	L	I	L	K	**T**	13
28	282	L	L	**V**	P	P	V	L	N	**P**	13
29	190	A	C	**D**	D	I	R	V	N	**V**	12
30	191	C	D	**D**	I	R	V	N	V	**V**	12
31	231	T	R	**E**	A	Q	A	K	A	**F**	12
32	268	R	R	**D**	S	P	L	P	V	**I**	12
33	270	D	S	**P**	L	P	V	I	L	**A**	12

HLA-A*0201 nonomers(SEQ ID NOS 1463-1569, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	287	V	**L**	N	P	I	V	Y	G	**V**	30
2	14	F	**I**	L	I	G	L	P	G	**L**	29
3	28	W	**L**	A	F	P	L	C	S	**L**	28
4	37	Y	**L**	I	A	V	L	G	N	**L**	28
5	222	L	**I**	L	K	T	V	L	G	**L**	28
6	66	C	**M**	L	S	G	I	D	I	**L**	26
7	108	S	**L**	S	G	M	E	S	T	**V**	26
8	181	C	**L**	H	Q	D	V	M	K	**L**	26
9	201	G	**L**	I	V	I	I	S	A	**I**	26
10	214	L	**L**	I	S	F	S	Y	L	**L**	26
11	275	V	**I**	L	A	N	I	Y	L	**L**	26
12	157	L	**M**	A	P	L	P	V	F	**I**	25
13	220	Y	**L**	L	I	L	K	T	V	**L**	25
14	276	I	**L**	A	N	I	Y	L	L	**V**	25
15	279	N	**I**	Y	L	L	V	P	P	**V**	25
16	138	L	**T**	L	P	R	V	T	K	**I**	24
17	213	S	**L**	L	I	S	F	S	Y	**L**	24
18	49	Y	**I**	V	R	T	E	H	S	**L**	23
19	143	V	**T**	K	I	G	V	A	A	**V**	23
20	188	K	**L**	A	C	D	D	I	R	**V**	23
21	198	V	**V**	Y	G	L	I	V	I	**I**	23
22	21	G	**L**	E	E	A	Q	F	W	**L**	22
23	40	A	**V**	L	G	N	L	T	I	**I**	22
24	206	I	**S**	A	I	G	L	D	S	**L**	22
25	11	A	**T**	Y	F	I	L	I	G	**L**	21
26	60	P	**M**	Y	I	F	L	C	M	**L**	21

HLA-A*0201 nonomers(SEQ ID NOS 1463-1569, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
27	135	A	**T**	V	L	T	L	P	R	**V**	21
28	160	P	**L**	P	V	F	I	K	Q	**L**	21
29	174	N	**I**	L	S	H	S	Y	C	**L**	21
30	207	S	**A**	I	G	L	D	S	L	**L**	21
31	272	P	**L**	P	V	I	L	A	N	**I**	21
32	283	L	**V**	P	P	V	L	N	P	**I**	21
33	67	M	**L**	S	G	I	D	I	L	**I**	20
34	101	L	**Q**	I	F	A	I	H	S	**L**	20
35	282	L	**L**	V	P	P	V	L	N	**P**	20
36	299	E	**I**	R	Q	R	I	L	R	**L**	20
37	304	I	**L**	R	L	F	H	V	A	**T**	20
38	39	I	**A**	V	L	G	N	L	T	**I**	19
39	45	L	**T**	I	I	Y	I	V	R	**T**	19
40	92	T	**T**	I	Q	F	D	A	C	**L**	19
41	110	S	**G**	M	E	S	T	V	L	**L**	19
42	127	A	**I**	C	H	P	L	R	H	**A**	19
43	132	L	**R**	H	A	T	V	L	T	**L**	19
44	149	A	**A**	V	V	R	G	A	A	**L**	19
45	155	A	**A**	L	M	A	P	L	P	**V**	19
46	156	A	**L**	M	A	P	L	P	V	**F**	19
47	203	I	**V**	I	I	S	A	I	G	**L**	19
48	208	A	**I**	G	L	D	S	L	L	**I**	19
49	216	I	**S**	F	S	Y	L	L	I	**L**	19
50	219	S	**Y**	L	L	I	L	K	T	**V**	19
51	221	L	**L**	I	L	K	T	V	L	**G**	19
52	223	I	**L**	K	T	V	L	G	L	**T**	19
53	17	I	**G**	L	P	G	L	E	E	**A**	18
54	33	L	**C**	S	L	Y	L	I	A	**V**	18
55	34	C	**S**	L	Y	L	I	A	V	**L**	18
56	38	L	**I**	A	V	L	G	N	L	**T**	18
57	43	G	**N**	L	T	I	I	Y	I	**V**	18
58	85	A	**I**	F	W	F	N	S	T	**T**	18
59	118	L	**A**	M	A	F	D	R	Y	**V**	18
60	194	I	**R**	V	N	V	V	Y	G	**L**	18
61	210	G	**L**	D	S	L	L	I	S	**F**	18
62	215	L	**I**	S	F	S	Y	L	L	**I**	18
63	246	V	**C**	A	V	F	I	F	Y	**V**	18
64	254	V	**P**	F	I	G	L	S	M	**V**	18
65	15	I	**L**	I	G	L	P	G	L	**E**	17
66	63	I	**F**	L	C	M	L	S	G	**I**	17
67	72	D	**I**	L	I	S	T	S	S	**M**	17
68	93	T	**I**	Q	F	D	A	C	L	**L**	17
69	98	A	**C**	L	L	Q	I	F	A	**I**	17
70	111	G	**M**	E	S	T	V	L	L	**A**	17
71	120	M	**A**	F	D	R	Y	V	A	**I**	17
72	167	Q	**L**	P	F	C	R	S	N	**I**	17
73	197	N	**V**	V	Y	G	L	I	V	**I**	17
74	226	T	**V**	L	G	L	T	R	E	**A**	17
75	281	Y	**L**	L	V	P	P	V	L	**N**	17

HLA-A*0201 nonomers(SEQ ID NOS 1463-1569, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
76	31	F	**P**	L	C	S	L	Y	L	**I**	16
77	56	S	**L**	H	E	P	M	Y	I	**F**	16
78	70	G	**I**	D	I	L	I	S	T	**S**	16
79	78	S	**S**	M	P	K	M	L	A	**I**	16
80	79	S	**M**	P	K	M	L	A	I	**F**	16
81	104	F	**A**	I	H	S	L	S	G	**M**	16
82	119	A	**M**	A	F	D	R	Y	V	**A**	16
83	144	T	**K**	I	G	V	A	A	V	**V**	16
84	147	G	**V**	A	A	V	V	R	G	**A**	16
85	186	V	**M**	K	L	A	C	D	D	**I**	16
86	230	L	**T**	R	E	A	Q	A	K	**A**	16
87	238	A	**F**	G	T	C	V	S	H	**V**	16
88	249	V	**F**	I	F	Y	V	P	F	**I**	16
89	302	Q	**R**	I	L	R	L	F	H	**V**	16
90	303	R	**I**	L	R	L	F	H	V	**A**	16
91	18	G	**L**	P	G	L	E	E	A	**Q**	15
92	35	S	**L**	Y	L	I	A	V	L	**G**	15
93	42	L	**G**	N	L	T	I	I	Y	**I**	15
94	46	T	**I**	I	Y	I	V	R	T	**E**	15
95	69	S	**G**	I	D	I	L	I	S	**T**	15
96	76	S	**T**	S	S	M	P	K	M	**L**	15
97	131	P	**L**	R	H	A	T	V	L	**T**	15
98	137	V	**L**	T	L	P	R	V	T	**K**	15
99	153	R	**G**	A	A	L	M	A	P	**L**	15
100	190	A	**C**	D	D	I	R	V	N	**V**	15
101	191	C	**D**	D	I	R	V	N	V	**V**	15
102	204	V	**I**	I	S	A	I	G	L	**D**	15
103	241	T	**C**	V	S	H	V	C	A	**V**	15
104	251	I	**F**	Y	V	P	F	I	G	**L**	15
105	269	R	**D**	S	P	L	P	V	I	**L**	15
106	280	I	**Y**	L	L	V	P	P	V	**L**	15
107	306	R	**L**	F	H	V	A	T	H	**A**	15

HLA A*0203 nonomers (SEQ ID NOS 1570-1594, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	148	V	A	**A**	V	V	R	G	A	**A**	14
2	119	A	M	**A**	F	D	R	Y	V	**A**	13
3	147	G	V	**A**	A	V	V	R	G	**A**	12
4	97	D	A	**C**	L	L	Q	I	F	**A**	11
5	127	A	I	**C**	H	P	L	R	H	**A**	10
6	3	D	P	**N**	G	N	E	S	S	**A**	9
7	17	I	G	**L**	P	G	L	E	E	**A**	9
8	22	L	E	**E**	A	Q	F	W	L	**A**	9
9	32	P	L	**C**	S	L	Y	L	I	**A**	9
10	77	T	S	**S**	M	P	K	M	L	**A**	9
11	90	N	S	**T**	T	I	Q	F	D	**A**	9

HLA A*0203 nonomers (SEQ ID NOS 1570-1594, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
12	111	G	M	**E**	S	T	V	L	L	**A**	9
13	113	E	S	**T**	V	L	L	A	M	**A**	9
14	141	P	R	**V**	T	K	I	G	V	**A**	9
15	142	R	V	**T**	K	I	G	V	A	**A**	9
16	151	V	V	**R**	G	A	A	L	M	**A**	9
17	182	L	H	**Q**	D	V	M	K	L	**A**	9
18	200	Y	G	**L**	I	V	I	I	S	**A**	9
19	226	T	V	**L**	G	L	T	R	E	**A**	9
20	228	L	G	**L**	T	R	E	A	Q	**A**	9
21	230	L	T	**R**	E	A	Q	A	K	**A**	9
22	240	G	T	**C**	V	S	H	V	C	**A**	9
23	270	D	S	**P**	L	P	V	I	L	**A**	9
24	303	R	I	**L**	R	L	F	H	V	**A**	9
25	306	R	L	**F**	H	V	A	T	H	**A**	9

HLA-A26 nonomers(SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Q	R	I	L	R	L	30
2	72	D	I	L	I	S	T	S	S	M	27
3	248	A	V	F	I	F	Y	V	P	F	27
4	210	G	L	D	S	L	L	I	S	F	26
5	14	F	I	L	I	G	L	P	G	L	24
6	56	S	L	H	E	P	M	Y	I	F	24
7	117	L	L	A	M	A	F	D	R	Y	24
8	222	L	I	L	K	T	V	L	G	L	24
9	245	H	V	C	A	V	F	I	F	Y	24
10	11	A	T	Y	F	I	L	I	G	L	23
11	37	Y	L	I	A	V	L	G	N	L	23
12	114	S	T	V	L	L	A	M	A	F	23
13	156	A	L	M	A	P	L	P	V	F	23
14	162	P	V	F	I	K	Q	L	P	F	23
15	181	C	L	H	Q	D	V	M	K	L	23
16	28	W	L	A	F	P	L	C	S	L	22
17	92	T	T	I	Q	F	D	A	C	L	22
18	160	P	L	P	V	F	I	K	Q	L	22
19	203	I	V	I	I	S	A	I	G	L	22
20	213	S	L	L	I	S	F	S	Y	L	22
21	275	V	I	L	A	N	I	Y	L	L	22
22	193	D	I	R	V	N	V	V	Y	G	21
23	242	C	V	S	H	V	C	A	V	F	21
24	76	S	T	S	S	M	P	K	M	L	20
25	253	Y	V	P	F	I	G	L	S	M	20
26	274	P	V	I	L	A	N	I	Y	L	20
27	23	E	E	A	Q	F	W	L	A	F	19
28	41	V	L	G	N	L	T	I	I	Y	19
29	49	Y	I	V	R	T	E	H	S	L	19

HLA-A26 nonomers(SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
30	150	A	V	V	R	G	A	A	L	M	19
31	174	N	I	L	S	H	S	Y	C	L	19
32	192	D	D	I	R	V	N	V	V	Y	19
33	214	L	L	I	S	F	S	Y	L	L	19
34	251	I	F	Y	V	P	F	I	G	L	19
35	8	E	S	S	A	T	Y	F	I	L	18
36	21	G	L	E	E	A	Q	F	W	L	18
37	45	L	T	I	I	Y	I	V	R	T	18
38	54	E	H	S	L	H	E	P	M	Y	18
39	59	E	P	M	Y	I	F	L	C	M	18
40	88	W	F	N	S	T	T	I	Q	F	18
41	93	T	I	Q	F	D	A	C	L	L	18
42	185	D	V	M	K	L	A	C	D	D	18
43	198	V	V	Y	G	L	I	V	I	I	18
44	62	Y	I	F	L	C	M	L	S	G	17
45	70	G	I	D	I	L	I	S	T	S	17
46	79	S	M	P	K	M	L	A	I	F	17
47	96	F	D	A	C	L	L	Q	I	F	17
48	104	F	A	I	H	S	L	S	G	M	17
49	138	L	T	L	P	R	V	T	K	I	17
50	143	V	T	K	I	G	V	A	A	V	17
51	204	V	I	I	S	A	I	G	L	D	17
52	212	D	S	L	L	I	S	F	S	Y	17
53	220	Y	L	L	I	L	K	T	V	L	17
54	256	F	I	G	L	S	M	V	H	R	17
55	283	L	V	P	P	V	L	N	P	I	17
56	29	L	A	F	P	L	C	S	L	Y	16
57	40	A	V	L	G	N	L	T	I	I	16
58	46	T	I	I	Y	I	V	R	T	E	16
59	52	R	T	E	H	S	L	H	E	P	16
60	75	I	S	T	S	S	M	P	K	M	16
61	91	S	T	T	I	Q	F	D	A	C	16
62	135	A	T	V	L	T	L	P	R	V	16
63	147	G	V	A	A	V	V	R	G	A	16
64	201	G	L	I	V	I	I	S	A	I	16
65	257	I	G	L	S	M	V	H	R	F	16
66	279	N	I	Y	L	L	V	P	P	V	16
67	30	A	F	P	L	C	S	L	Y	L	15
68	101	L	Q	I	F	A	I	H	S	L	15
69	115	T	V	L	L	A	M	A	F	D	15
70	127	A	I	C	H	P	L	R	H	A	15
71	153	R	G	A	A	L	M	A	P	L	15
72	163	V	F	I	K	Q	L	P	F	C	15
73	215	L	I	S	F	S	Y	L	L	I	15
74	216	I	S	F	S	Y	L	L	I	L	15
75	225	K	T	V	L	G	L	T	R	E	15
76	272	P	L	P	V	I	L	A	N	I	15
77	282	L	L	V	P	P	V	L	N	P	15
78	286	P	V	L	N	P	I	V	Y	G	15

HLA-A26 nonomers(SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
79	287	V	L	N	P	I	V	Y	G	V	15
80	296	K	T	K	E	I	R	Q	R	I	15
81	303	R	I	L	R	L	F	H	V	A	15

HLA-A3 nonomers(SEQ ID NOS 1676-1747, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	137	V	**L**	T	L	P	R	V	T	**K**	30
2	229	G	**L**	T	R	E	A	Q	A	**K**	27
3	145	K	**I**	G	V	A	A	V	V	**R**	26
4	150	A	**V**	V	R	G	A	A	L	**M**	24
5	290	P	**I**	V	Y	G	V	K	T	**K**	24
6	35	S	**L**	Y	L	I	A	V	L	**G**	23
7	156	A	**L**	M	A	P	L	P	V	**F**	23
8	47	I	**I**	Y	I	V	R	T	E	**H**	22
9	50	I	**V**	R	T	E	H	S	L	**H**	22
10	142	R	**V**	T	K	I	G	V	A	**A**	22
11	151	V	**V**	R	G	A	A	L	M	**A**	22
12	242	C	**V**	S	H	V	C	A	V	**F**	22
13	248	A	**V**	F	I	F	Y	V	P	**F**	22
14	116	V	**L**	L	A	M	A	F	D	**R**	21
15	192	D	**D**	I	R	V	N	V	V	**Y**	21
16	303	R	**I**	L	R	L	F	H	V	**A**	21
17	304	I	**L**	R	L	F	H	V	A	**T**	21
18	108	S	**L**	S	G	M	E	S	T	**V**	20
19	198	V	**V**	Y	G	L	I	V	I	**I**	20
20	291	I	**V**	Y	G	V	K	T	K	**E**	20
21	15	I	**L**	I	G	L	P	G	L	**E**	19
22	44	N	**L**	T	I	I	Y	I	V	**R**	19
23	73	I	**L**	I	S	T	S	S	M	**P**	19
24	74	L	**I**	S	T	S	S	M	P	**K**	19
25	99	C	**L**	L	Q	I	F	A	I	**H**	19
26	162	P	**V**	F	I	K	Q	L	P	**F**	19
27	203	I	**V**	I	I	S	A	I	G	**L**	19
28	221	L	**L**	I	L	K	T	V	L	**G**	19
29	245	H	**V**	C	A	V	F	I	F	**Y**	19
30	306	R	**L**	F	H	V	A	T	H	**A**	19
31	40	A	**V**	L	G	N	L	T	I	**I**	18
32	85	A	**I**	F	W	F	N	S	T	**T**	18
33	205	I	**I**	S	A	I	G	L	D	**S**	18
34	220	Y	**L**	L	I	L	K	T	V	**L**	18
35	253	Y	**V**	P	F	I	G	L	S	**M**	18
36	37	Y	**L**	I	A	V	L	G	N	**L**	17
37	41	V	**L**	G	N	L	T	I	I	**Y**	17
38	117	L	**L**	A	M	A	F	D	R	**Y**	17
39	131	P	**L**	R	H	A	T	V	L	**T**	17
40	136	T	**V**	L	T	L	P	R	V	**T**	17

HLA-A3 nonomers(SEQ ID NOS 1676-1747, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
41	180	Y	**C**	L	H	Q	D	V	M	**K**	17
42	201	G	**L**	I	V	I	I	S	A	**I**	17
43	213	S	**L**	L	I	S	F	S	Y	**L**	17
44	256	F	**I**	G	L	S	M	V	H	**R**	17
45	261	M	**V**	H	R	F	S	K	R	**R**	17
46	276	I	**L**	A	N	I	Y	L	L	**V**	17
47	281	Y	**L**	L	V	P	P	V	L	**N**	17
48	286	P	**V**	L	N	P	I	V	Y	**G**	17
49	288	L	**N**	P	I	V	Y	G	V	**K**	17
50	309	H	**V**	A	T	H	A	S	E	**P**	17
51	1	M	**V**	D	P	N	G	N	E	**S**	16
52	56	S	**L**	H	E	P	M	Y	I	**F**	16
53	70	G	**I**	D	I	L	I	S	T	**S**	16
54	72	D	**I**	L	I	S	T	S	S	**M**	16
55	115	T	**V**	L	L	A	M	A	F	**D**	16
56	125	Y	**V**	A	I	C	H	P	L	**R**	16
57	144	T	**K**	I	G	V	A	A	V	**V**	16
58	167	Q	**L**	P	F	C	R	S	N	**I**	16
59	175	I	**L**	S	H	S	Y	C	L	**H**	16
60	195	R	**V**	N	V	V	Y	G	L	**I**	16
61	197	N	**V**	V	Y	G	L	I	V	**I**	16
62	210	G	**L**	D	S	L	L	I	S	**F**	16
63	282	L	**L**	V	P	P	V	L	N	**P**	16
64	299	E	**I**	R	Q	R	I	L	R	**L**	16
65	301	R	**Q**	R	I	L	R	L	F	**H**	16
66	16	L	**I**	G	L	P	G	L	E	**E**	15
67	46	T	**I**	I	Y	I	V	R	T	**E**	15
68	102	Q	**I**	F	A	I	H	S	L	**S**	15
69	193	D	**I**	R	V	N	V	V	Y	**G**	15
70	208	A	**I**	G	L	D	S	L	L	**I**	15
71	223	I	**L**	K	T	V	L	G	L	**T**	15
72	237	K	**A**	F	G	T	C	V	S	**H**	15

HLA-B*0702 nonomers(SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	130	H	**P**	L	R	H	A	T	V	**L**	22
2	59	E	**P**	M	Y	I	F	L	C	**M**	21
3	168	L	**P**	F	C	R	S	N	I	**L**	20
4	289	N	**P**	I	V	Y	G	V	K	**T**	19
5	3	D	**P**	N	G	N	E	S	S	**A**	18
6	19	L	**P**	G	L	E	E	A	Q	**F**	18
7	140	L	**P**	R	V	T	K	I	G	**V**	18
8	284	V	**P**	P	V	L	N	P	I	**V**	17
9	31	F	**P**	L	C	S	L	Y	L	**I**	16
10	254	V	**P**	F	I	G	L	S	M	**V**	16
11	269	R	**D**	S	P	L	P	V	I	**L**	16

HLA-B*0702 nonomers(SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
12	149	A	**A**	V	V	R	G	A	A	**L**	15
13	153	R	**G**	A	A	L	M	A	P	**L**	15
14	156	A	**L**	M	A	P	L	P	V	**F**	15
15	251	I	**F**	Y	V	P	F	I	G	**L**	15
16	299	E	**I**	R	Q	R	I	L	R	**L**	15
17	8	E	**S**	S	A	T	Y	F	I	**L**	14
18	28	W	**L**	A	F	P	L	C	S	**L**	14
19	30	A	**F**	P	L	C	S	L	Y	**L**	14
20	110	S	**G**	M	E	S	T	V	L	**L**	14
21	132	L	**R**	H	A	T	V	L	T	**L**	14
22	159	A	**P**	L	P	V	F	I	K	**Q**	14
23	222	L	**I**	L	K	T	V	L	G	**L**	14
24	271	S	**P**	L	P	V	I	L	A	**N**	14
25	25	A	**Q**	F	W	L	A	F	P	**L**	13
26	109	L	**S**	G	M	E	S	T	V	**L**	13
27	124	R	**Y**	V	A	I	C	H	P	**L**	13
28	216	I	**S**	F	S	Y	L	L	I	**L**	13
29	268	R	**R**	D	S	P	L	P	V	**I**	13
30	280	I	**Y**	L	L	V	P	P	V	**L**	13
31	11	A	**T**	Y	F	I	L	I	G	**L**	12
32	34	C	**S**	L	Y	L	I	A	V	**L**	12
33	57	L	**H**	E	P	M	Y	I	F	**L**	12
34	76	S	**T**	S	S	M	P	K	M	**L**	12
35	142	R	**V**	T	K	I	G	V	A	**A**	12
36	151	V	**V**	R	G	A	A	L	M	**A**	12
37	190	A	**C**	D	D	I	R	V	N	**V**	12
38	194	I	**R**	V	N	V	V	Y	G	**L**	12
39	206	I	**S**	A	I	G	L	D	S	**L**	12
40	207	S	**A**	I	G	L	D	S	L	**L**	12
41	220	Y	**L**	L	I	L	K	T	V	**L**	12
42	267	K	**R**	R	D	S	P	L	P	**V**	12
43	304	I	**L**	R	L	F	H	V	A	**T**	12
44	14	F	**I**	L	I	G	L	P	G	**L**	11
45	23	E	**E**	A	Q	F	W	L	A	**F**	11
46	37	Y	**L**	I	A	V	L	G	N	**L**	11
47	40	A	**V**	L	G	N	L	T	I	**I**	11
48	77	T	**S**	S	M	P	K	M	L	**A**	11
49	78	S	**S**	M	P	K	M	L	A	**I**	11
50	80	M	**P**	K	M	L	A	I	F	**W**	11
51	92	T	**T**	I	Q	F	D	A	C	**L**	11
52	112	M	**E**	S	T	V	L	L	A	**M**	11
53	119	A	**M**	A	F	D	R	Y	V	**A**	11
54	127	A	**I**	C	H	P	L	R	H	**A**	11
55	131	P	**L**	R	H	A	T	V	L	**T**	11
56	155	A	**A**	L	M	A	P	L	P	**V**	11
57	157	L	**M**	A	P	L	P	V	F	**I**	11
58	181	C	**L**	H	Q	D	V	M	K	**L**	11
59	203	I	**V**	I	I	S	A	I	G	**L**	11
60	208	A	**I**	G	L	D	S	L	L	**I**	11

HLA-B*0702 nonomers(SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
61	213	S	**L**	L	I	S	F	S	Y	**L**	11
62	248	A	**V**	F	I	F	Y	V	P	**F**	11
63	265	F	**S**	K	R	R	D	S	P	**L**	11
64	275	V	**I**	L	A	N	I	Y	L	**L**	11
65	285	P	**P**	V	L	N	P	I	V	**Y**	11

HLA-B*08 nonomers(SEQ ID NOS 1813-1847, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	**R**	Q	**R**	I	L	R	**L**	31
2	265	F	S	**K**	R	**R**	D	S	P	**L**	29
3	149	A	A	**V**	V	**R**	G	A	A	**L**	24
4	168	L	P	**F**	C	**R**	S	N	I	**L**	24
5	294	G	V	**K**	T	**K**	E	I	R	**Q**	21
6	120	M	A	**F**	D	**R**	Y	V	A	**I**	20
7	292	V	Y	**G**	V	**K**	T	K	E	**I**	20
8	21	G	L	**E**	E	**A**	Q	F	W	**L**	19
9	78	S	S	**M**	P	**K**	M	L	A	**I**	19
10	160	P	L	**P**	V	**F**	I	K	Q	**L**	19
11	186	V	M	**K**	L	**A**	C	D	D	**I**	18
12	213	S	L	**L**	I	**S**	F	S	Y	**L**	18
13	221	L	L	**I**	L	**K**	T	V	L	**G**	18
14	296	K	T	**K**	E	**I**	R	Q	R	**I**	18
15	297	T	K	**E**	I	**R**	Q	R	I	**L**	18
16	130	H	P	**L**	R	**H**	A	T	V	**L**	17
17	181	C	L	**H**	Q	**D**	V	M	K	**L**	17
18	223	I	L	**K**	T	**V**	L	G	L	**T**	17
19	28	W	L	**A**	F	**P**	L	C	S	**L**	16
20	37	Y	L	**I**	A	**V**	L	G	N	**L**	16
21	56	S	L	**H**	E	**P**	M	Y	I	**F**	16
22	80	M	P	**K**	M	**L**	A	I	F	**W**	16
23	162	P	V	**F**	I	**K**	Q	L	P	**F**	16
24	201	G	L	**I**	V	**I**	I	S	A	**I**	16
25	207	S	A	**I**	G	**L**	D	S	L	**L**	16
26	214	L	L	**I**	S	**F**	S	Y	L	**L**	16
27	220	Y	L	**L**	I	**L**	K	T	V	**L**	16
28	233	E	A	**Q**	A	**K**	A	F	G	**T**	16
29	275	V	I	**L**	A	**N**	I	Y	L	**L**	16
30	304	I	L	**R**	L	**F**	H	V	A	**T**	16
31	14	F	I	**L**	I	**G**	L	P	G	**L**	15
32	110	S	G	**M**	E	**S**	T	V	L	**L**	15
33	138	L	T	**L**	P	**R**	V	T	K	**I**	15
34	164	F	I	**K**	Q	**L**	P	F	C	**R**	15
35	222	L	I	**L**	K	**T**	V	L	G	**L**	15

HLA-B*1510 nonomers(SEQ ID NOS 1848-1890, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	57	L	**H**	E	P	M	Y	I	F	**L**	23
2	244	S	**H**	V	C	A	V	F	I	**F**	17
3	269	R	**D**	S	P	L	P	V	I	**L**	16
4	280	I	**Y**	L	L	V	P	P	V	**L**	16
5	262	V	**H**	R	F	S	K	R	R	**D**	15
6	299	E	**I**	R	Q	R	I	L	R	**L**	15
7	106	I	**H**	S	L	S	G	M	E	**S**	14
8	206	I	**S**	A	I	G	L	D	S	**L**	14
9	220	Y	**L**	L	I	L	K	T	V	**L**	14
10	251	I	**F**	Y	V	P	F	I	G	**L**	14
11	297	T	**K**	E	I	R	Q	R	I	**L**	14
12	21	G	**L**	E	E	A	Q	F	W	**L**	13
13	34	C	**S**	L	Y	L	I	A	V	**L**	13
14	54	E	**H**	S	L	H	E	P	M	**Y**	13
15	110	S	**G**	M	E	S	T	V	L	**L**	13
16	194	I	**R**	V	N	V	V	Y	G	**L**	13
17	8	E	**S**	S	A	T	Y	F	I	**L**	12
18	14	F	**I**	L	I	G	L	P	G	**L**	12
19	28	W	**L**	A	F	P	L	C	S	**L**	12
20	66	C	**M**	L	S	G	I	D	I	**L**	12
21	76	S	**T**	S	S	M	P	K	M	**L**	12
22	92	T	**T**	I	Q	F	D	A	C	**L**	12
23	109	L	**S**	G	M	E	S	T	V	**L**	12
24	130	H	**P**	L	R	H	A	T	V	**L**	12
25	132	L	**R**	H	A	T	V	L	T	**L**	12
26	149	A	**A**	V	V	R	G	A	A	**L**	12
27	153	R	**G**	A	A	L	M	A	P	**L**	12
28	160	P	**L**	P	V	F	I	K	Q	**L**	12
29	181	C	**L**	H	Q	D	V	M	K	**L**	12
30	182	L	**H**	Q	D	V	M	K	L	**A**	12
31	203	I	**V**	I	I	S	A	I	G	**L**	12
32	216	I	**S**	F	S	Y	L	L	I	**L**	12
33	222	L	**I**	L	K	T	V	L	G	**L**	12
34	275	V	**I**	L	A	N	I	Y	L	**L**	12
35	37	Y	**L**	I	A	V	L	G	N	**L**	11
36	49	Y	**I**	V	R	T	E	H	S	**L**	11
37	93	T	**I**	Q	F	D	A	C	L	**L**	11
38	101	L	**Q**	I	F	A	I	H	S	**L**	11
39	129	C	**H**	P	L	R	H	A	T	**V**	11
40	133	R	**H**	A	T	V	L	T	L	**P**	11
41	177	S	**H**	S	Y	C	L	H	Q	**D**	11
42	207	S	**A**	I	G	L	D	S	L	**L**	11
43	257	I	**G**	L	S	M	V	H	R	**F**	11

HLA-B*2705 nonomers(SEQ ID NOS 1891-2008, respectively in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	score

HLA-B*2705 nonomers(SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	**R**	V	N	V	V	Y	G	**L**	25
2	268	R	**R**	D	S	P	L	P	V	**I**	24
3	132	L	**R**	H	A	T	V	L	T	**L**	23
4	300	I	**R**	Q	R	I	L	R	L	**F**	23
5	305	L	**R**	L	F	H	V	A	T	**H**	23
6	231	T	**R**	E	A	Q	A	K	A	**F**	21
7	34	C	**S**	L	Y	L	I	A	V	**L**	18
8	299	E	**I**	R	Q	R	I	L	R	**L**	18
9	6	G	**N**	E	S	S	A	T	Y	**F**	17
10	66	C	**M**	L	S	G	I	D	I	**L**	17
11	162	P	**V**	F	I	K	Q	L	P	**F**	17
12	207	S	**A**	I	G	L	D	S	L	**L**	17
13	210	G	**L**	D	S	L	L	I	S	**F**	17
14	220	Y	**L**	L	I	L	K	T	V	**L**	17
15	237	K	**A**	F	G	T	C	V	S	**H**	17
16	269	R	**D**	S	P	L	P	V	I	**L**	17
17	280	I	**Y**	L	L	V	P	P	V	**L**	17
18	295	V	**K**	T	K	E	I	R	Q	**R**	17
19	11	A	**T**	Y	F	I	L	I	G	**L**	16
20	14	F	**I**	L	I	G	L	P	G	**L**	16
21	21	G	**L**	E	E	A	Q	F	W	**L**	16
22	25	A	**Q**	F	W	L	A	F	P	**L**	16
23	37	Y	**L**	I	A	V	L	G	N	**L**	16
24	92	T	**T**	I	Q	F	D	A	C	**L**	16
25	101	L	**Q**	I	F	A	I	H	S	**L**	16
26	124	R	**Y**	V	A	I	C	H	P	**L**	16
27	130	H	**P**	L	R	H	A	T	V	**L**	16
28	141	P	**R**	V	T	K	I	G	V	**A**	16
29	153	R	**G**	A	A	L	M	A	P	**L**	16
30	181	C	**L**	H	Q	D	V	M	K	**L**	16
31	201	G	**L**	I	V	I	I	S	A	**I**	16
32	203	I	**V**	I	I	S	A	I	G	**L**	16
33	216	I	**S**	F	S	Y	L	L	I	**L**	16
34	222	L	**I**	L	K	T	V	L	G	**L**	16
35	255	P	**F**	I	G	L	S	M	V	**H**	16
36	257	I	**G**	L	S	M	V	H	R	**F**	16
37	275	V	**I**	L	A	N	I	Y	L	**L**	16
38	47	I	**I**	Y	I	V	R	T	E	**H**	15
39	109	L	**S**	G	M	E	S	T	V	**L**	15
40	114	S	**T**	V	L	L	A	M	A	**F**	15
41	123	D	**R**	Y	V	A	I	C	H	**P**	15
42	145	K	**I**	G	V	A	A	V	V	**R**	15
43	156	A	**L**	M	A	P	L	P	V	**F**	15
44	168	L	**P**	F	C	R	S	N	I	**L**	15
45	172	R	**S**	N	I	L	S	H	S	**Y**	15
46	198	V	**V**	Y	G	L	I	V	I	**I**	15
47	206	I	**S**	A	I	G	L	D	S	**L**	15
48	229	G	**L**	T	R	E	A	Q	A	**K**	15
49	248	A	**V**	F	I	F	Y	V	P	**F**	15

HLA-B*2705 nonomers(SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
50	251	I	**F**	Y	V	P	F	I	G	**L**	15
51	274	P	**V**	I	L	A	N	I	Y	**L**	15
52	290	P	**I**	V	Y	G	V	K	T	**K**	15
53	298	K	**E**	I	R	Q	R	I	L	**R**	15
54	19	L	**P**	G	L	E	E	A	Q	**F**	14
55	29	L	**A**	F	P	L	C	S	L	**Y**	14
56	30	A	**F**	P	L	C	S	L	Y	**L**	14
57	39	I	**A**	V	L	G	N	L	T	**I**	14
58	40	A	**V**	L	G	N	L	T	I	**I**	14
59	79	S	**M**	P	K	M	L	A	I	**F**	14
60	81	P	**K**	M	L	A	I	F	W	**F**	14
61	99	C	**L**	L	Q	I	F	A	I	**H**	14
62	137	V	**L**	T	L	P	R	V	T	**K**	14
63	138	L	**T**	L	P	R	V	T	K	**I**	14
64	150	A	**V**	V	R	G	A	A	L	**M**	14
65	160	P	**L**	P	V	F	I	K	Q	**L**	14
66	174	N	**I**	L	S	H	S	Y	C	**L**	14
67	180	Y	**C**	L	H	Q	D	V	M	**K**	14
68	192	D	**D**	I	R	V	N	V	V	**Y**	14
69	212	D	**S**	L	L	I	S	F	S	**Y**	14
70	213	S	**L**	L	I	S	F	S	Y	**L**	14
71	214	L	**L**	I	S	F	S	Y	L	**L**	14
72	260	S	**M**	V	H	R	F	S	K	**R**	14
73	263	H	**R**	F	S	K	R	R	D	**S**	14
74	267	K	**R**	R	D	S	P	L	P	**V**	14
75	293	Y	**G**	V	K	T	K	E	I	**R**	14
76	301	R	**Q**	R	I	L	R	L	F	**H**	14
77	302	Q	**R**	I	L	R	L	F	H	**V**	14
78	5	N	**G**	N	E	S	S	A	T	**Y**	13
79	23	E	**E**	A	Q	F	W	L	A	**F**	13
80	28	W	**L**	A	F	P	L	C	S	**L**	13
81	44	N	**L**	T	I	I	Y	I	V	**R**	13
82	51	V	**R**	T	E	H	S	L	H	**E**	13
83	56	S	**L**	H	E	P	M	Y	I	**F**	13
84	60	P	**M**	Y	I	F	L	C	M	**L**	13
85	72	D	**I**	L	I	S	T	S	S	**M**	13
86	74	L	**I**	S	T	S	S	M	P	**K**	13
87	75	I	**S**	T	S	S	M	P	K	**M**	13
88	98	A	**C**	L	L	Q	I	F	A	**I**	13
89	104	F	**A**	I	H	S	L	S	G	**M**	13
90	110	S	**G**	M	E	S	T	V	L	**L**	13
91	116	V	**L**	L	A	M	A	F	D	**R**	13
92	126	V	**A**	I	C	H	P	L	R	**H**	13
93	149	A	**A**	V	V	R	G	A	A	**L**	13
94	158	M	**A**	P	L	P	V	F	I	**K**	13
95	164	F	**I**	K	Q	L	P	F	C	**R**	13
96	170	F	**C**	R	S	N	I	L	S	**H**	13
97	171	C	**R**	S	N	I	L	S	H	**S**	13
98	187	M	**K**	L	A	C	D	D	I	**R**	13

HLA-B*2705 nonomers(SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
99	217	S	**F**	S	Y	L	L	I	L	**K**	13
100	224	L	**K**	T	V	L	G	L	T	**R**	13
101	242	C	**V**	S	H	V	C	A	V	**F**	13
102	256	F	**I**	G	L	S	M	V	H	**R**	13
103	261	M	**V**	H	R	F	S	K	R	**R**	13
104	49	Y	**I**	V	R	T	E	H	S	**L**	12
105	57	L	**H**	E	P	M	Y	I	F	**L**	12
106	88	W	**F**	N	S	T	T	I	Q	**F**	12
107	96	F	**D**	A	C	L	L	Q	I	**F**	12
108	134	H	**A**	T	V	L	T	L	P	**R**	12
109	152	V	**R**	G	A	A	L	M	A	**P**	12
110	179	S	**Y**	C	L	H	Q	D	V	**M**	12
111	197	N	**V**	V	Y	G	L	I	V	**I**	12
112	244	S	**H**	V	C	A	V	F	I	**F**	12
113	265	F	**S**	K	R	R	D	S	P	**L**	12
114	273	L	**P**	V	I	L	A	N	I	**Y**	12
115	285	P	**P**	V	L	N	P	I	V	**Y**	12
116	288	L	**N**	P	I	V	Y	G	V	**K**	12
117	296	K	**T**	K	E	I	R	Q	R	**I**	12
118	297	T	**K**	E	I	R	Q	R	I	**L**	12

HLA-B*2709 nonomers(SEQ ID NOS 2009-2063, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	R	V	N	V	V	Y	G	L	24
2	268	R	R	D	S	P	L	P	V	I	24
3	132	L	R	H	A	T	V	L	T	L	22
4	267	K	R	R	D	S	P	L	P	V	21
5	300	I	R	Q	R	I	L	R	L	F	20
6	231	T	R	E	A	Q	A	K	A	F	19
7	302	Q	R	I	L	R	L	F	H	V	19
8	124	R	Y	V	A	I	C	H	P	L	16
9	269	R	D	S	P	L	P	V	I	L	16
10	43	G	N	L	T	I	I	Y	I	V	15
11	216	I	S	F	S	Y	L	L	I	L	15
12	11	A	T	Y	F	I	L	I	G	L	14
13	25	A	Q	F	W	L	A	F	P	L	14
14	153	R	G	A	A	L	M	A	P	L	14
15	174	N	I	L	S	H	S	Y	C	L	14
16	222	L	I	L	K	T	V	L	G	L	14
17	257	I	G	L	S	M	V	H	R	F	14
18	280	I	Y	L	L	V	P	P	V	L	14
19	6	G	N	E	S	S	A	T	Y	F	13
20	14	F	I	L	I	G	L	P	G	L	13
21	21	G	L	E	E	A	Q	F	W	L	13
22	66	C	M	L	S	G	I	D	I	L	13

HLA-B*2709 nonomers(SEQ ID NOS 2009-2063, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
23	130	H	P	L	R	H	A	T	V	L	13
24	201	G	L	I	V	I	I	S	A	I	13
25	203	I	V	I	I	S	A	I	G	L	13
26	214	L	L	I	S	F	S	Y	L	L	13
27	251	I	F	Y	V	P	F	I	G	L	13
28	263	H	R	F	S	K	R	R	D	S	13
29	275	V	I	L	A	N	I	Y	L	L	13
30	305	L	R	L	F	H	V	A	T	H	13
31	30	A	F	P	L	C	S	L	Y	L	12
32	34	C	S	L	Y	L	I	A	V	L	12
33	37	Y	L	I	A	V	L	G	N	L	12
34	51	V	R	T	E	H	S	L	H	E	12
35	60	P	M	Y	I	F	L	C	M	L	12
36	75	I	S	T	S	S	M	P	K	M	12
37	93	T	I	Q	F	D	A	C	L	L	12
38	123	D	R	Y	V	A	I	C	H	P	12
39	135	A	T	V	L	T	L	P	R	V	12
40	138	L	T	L	P	R	V	T	K	I	12
41	149	A	A	V	V	R	G	A	A	L	12
42	155	A	A	L	M	A	P	L	P	V	12
43	168	L	P	F	C	R	S	N	I	L	12
44	181	C	L	H	Q	D	V	M	K	L	12
45	188	K	L	A	C	D	D	I	R	V	12
46	190	A	C	D	D	I	R	V	N	V	12
47	195	R	V	N	V	V	Y	G	L	I	12
48	210	G	L	D	S	L	L	I	S	F	12
49	213	S	L	L	I	S	F	S	Y	L	12
50	220	Y	L	L	I	L	K	T	V	L	12
51	248	A	V	F	I	F	Y	V	P	F	12
52	279	N	I	Y	L	L	V	P	P	V	12
53	287	V	L	N	P	I	V	Y	G	V	12
54	296	K	T	K	E	I	R	Q	R	I	12
55	299	E	I	R	Q	R	I	L	R	L	12

HLA-B*5101 nonomers(SEQ ID NOS 2064-2132, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	39	I	**A**	V	L	G	N	L	T	**I**	26
2	31	F	**P**	L	C	S	L	Y	L	**I**	25
3	120	M	**A**	F	D	R	Y	V	A	**I**	24
4	130	H	**P**	L	R	H	A	T	V	**L**	23
5	118	L	**A**	M	A	F	D	R	Y	**V**	22
6	140	L	**P**	R	V	T	K	I	G	**V**	22
7	155	A	**A**	L	M	A	P	L	P	**V**	22
8	42	L	**G**	N	L	T	I	I	Y	**I**	21
9	254	V	**P**	F	I	G	L	S	M	**V**	21
10	284	V	**P**	P	V	L	N	P	I	**V**	21

HLA-B*5101 nonomers(SEQ ID NOS 2064-2132, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
11	168	L	**P**	F	C	R	S	N	I	**L**	20
12	235	Q	**A**	K	A	F	G	T	C	**V**	20
13	138	**L**	**T**	L	P	R	V	T	K	**I**	19
14	159	A	**P**	L	P	V	F	I	K	**Q**	18
15	189	L	**A**	C	D	D	I	R	V	**N**	18
16	198	V	**V**	Y	G	L	I	V	I	**I**	18
17	277	L	**A**	N	I	Y	L	L	V	**P**	18
18	207	S	**A**	I	G	L	D	S	L	**L**	17
19	283	L	**V**	P	P	V	L	N	P	**I**	17
20	63	I	**F**	L	C	M	L	S	G	**I**	16
21	86	I	**F**	W	F	N	S	T	T	**I**	16
22	110	S	**G**	M	E	S	T	V	L	**L**	16
23	144	T	**K**	I	G	V	A	A	V	**V**	16
24	149	A	**A**	V	V	R	G	A	A	**L**	16
25	197	N	**V**	V	Y	G	L	I	V	**I**	16
26	271	S	**P**	L	P	V	I	L	A	**N**	16
27	280	I	**Y**	L	L	V	P	P	V	**L**	16
28	3	D	**P**	N	G	N	E	S	S	**A**	15
29	40	A	**V**	L	G	N	L	T	I	**I**	15
30	97	D	**A**	C	L	L	Q	I	F	**A**	15
31	132	L	**R**	H	A	T	V	L	T	**L**	15
32	222	L	**I**	L	K	T	V	L	G	**L**	15
33	279	N	**I**	Y	L	L	V	P	P	**V**	15
34	285	P	**P**	V	L	N	P	I	V	**Y**	15
35	289	N	**P**	I	V	Y	G	V	K	**T**	15
36	9	S	**S**	A	T	Y	F	I	L	**I**	14
37	65	L	**C**	M	L	S	G	I	D	**I**	14
38	84	L	**A**	I	F	W	F	N	S	**T**	14
39	126	V	**A**	I	C	H	P	L	R	**H**	14
40	157	L	**M**	A	P	L	P	V	F	**I**	14
41	158	M	**A**	P	L	P	V	F	I	**K**	14
42	191	C	**D**	D	I	R	V	N	V	**V**	14
43	200	Y	**G**	L	I	V	I	I	S	**A**	14
44	209	I	**G**	L	D	S	L	L	I	**S**	14
45	215	L	**I**	S	F	S	Y	L	L	**I**	14
46	219	S	**Y**	L	L	I	L	K	T	**V**	14
47	220	Y	**L**	L	I	L	K	T	V	**L**	14
48	237	K	**A**	F	G	T	C	V	S	**H**	14
49	247	C	**A**	V	F	I	F	Y	V	**P**	14
50	249	V	**F**	I	F	Y	V	P	F	**I**	14
51	251	I	**F**	Y	V	P	F	I	G	**L**	14
52	257	I	**G**	L	S	M	V	H	R	**F**	14
53	268	R	**R**	D	S	P	L	P	V	**I**	14
54	273	L	**P**	V	I	L	A	N	I	**Y**	14
55	29	L	**A**	F	P	L	C	S	L	**Y**	13
56	33	L	**C**	S	L	Y	L	I	A	**V**	13
57	55	H	**S**	L	H	E	P	M	Y	**I**	13
58	67	M	**L**	S	G	I	D	I	L	**I**	13
59	80	M	**P**	K	M	L	A	I	F	**W**	13

HLA-B*5101 nonomers(SEQ ID NOS 2064-2132, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
60	95	Q	**F**	D	A	C	L	L	Q	**I**	13
61	98	A	**C**	L	L	Q	I	F	A	**I**	13
62	104	F	**A**	I	H	S	L	S	G	**M**	13
63	146	I	**G**	V	A	A	V	V	R	**G**	13
64	148	V	**A**	A	V	V	R	G	A	**A**	13
65	153	R	**G**	A	A	L	M	A	P	**L**	13
66	233	E	**A**	Q	A	K	A	F	G	**T**	13
67	243	V	**S**	H	V	C	A	V	F	**I**	13
68	292	V	**Y**	G	V	K	T	K	E	**I**	13
69	296	K	**T**	K	E	I	R	Q	R	**I**	13

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Please replace Table XXVII, beginning at page 201, line 1, with the following rewritten Table XXVII:

--Table XXVII:
HLA Class I decamers

HLA-A1 decamers(SEQ ID NOS 2133-2153, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	191	C	D	**D**	I	R	V	N	V	**V**	Y	27
2	244	S	H	**V**	C	A	V	F	I	**F**	Y	24
3	40	A	V	**L**	G	N	L	T	I	**I**	Y	21
4	284	V	P	**P**	V	L	N	P	I	**V**	Y	21
5	116	V	L	**L**	A	M	A	F	D	**R**	Y	20
6	28	W	L	**A**	F	P	L	C	S	**L**	Y	18
7	297	T	K	**E**	I	R	Q	R	I	**L**	R	17
8	21	G	L	**E**	E	A	Q	F	W	**L**	A	16
9	22	L	E	**E**	A	Q	F	W	L	**A**	F	16
10	52	R	T	**E**	H	S	L	H	E	**P**	M	16
11	53	T	E	**H**	S	L	H	E	P	**M**	Y	16
12	57	L	H	**E**	P	M	Y	I	F	**L**	C	16
13	111	G	M	**E**	S	T	V	L	L	**A**	M	16
14	272	P	L	**P**	V	I	L	A	N	**I**	Y	16
15	1	M	V	**D**	P	N	G	N	E	**S**	S	15
16	4	P	N	**G**	N	E	S	S	A	**T**	Y	15
17	121	A	F	**D**	R	Y	V	A	I	**C**	H	15
18	171	C	R	**S**	N	I	L	S	H	**S**	Y	15
19	211	L	D	**S**	L	L	I	S	F	**S**	Y	15
20	8	E	S	**S**	A	T	Y	F	I	**L**	I	13
21	190	A	C	**D**	D	I	R	V	N	**V**	V	13

HLA-A*0201 decamers(SEQ ID NOS 2154-2253, respectively in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score

HLA-A*0201 decamers(SEQ ID NOS 2154-2253, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	221	L	**L**	I	L	K	T	V	L	**G**	L	30
2	100	L	**L**	Q	I	F	A	I	H	**S**	L	29
3	282	L	**L**	V	P	P	V	L	N	**P**	I	27
4	205	I	**I**	S	A	I	G	L	D	**S**	L	26
5	213	S	**L**	L	I	S	F	S	Y	**L**	L	25
6	56	S	**L**	H	E	P	M	Y	I	**F**	L	24
7	62	Y	**I**	F	L	C	M	L	S	**G**	I	24
8	108	S	**L**	S	G	M	E	S	T	**V**	L	24
9	117	L	**L**	A	M	A	F	D	R	**Y**	V	24
10	131	P	**L**	R	H	A	T	V	L	**T**	L	24
11	137	V	**L**	T	L	P	R	V	T	**K**	I	24
12	215	L	**I**	S	F	S	Y	L	L	**I**	L	24
13	38	L	**I**	A	V	L	G	N	L	**T**	I	23
14	41	V	**L**	G	N	L	T	I	I	**Y**	I	23
15	156	A	**L**	M	A	P	L	P	V	**F**	I	23
16	193	D	**I**	R	V	N	V	V	Y	**G**	L	23
17	214	L	**L**	I	S	F	S	Y	L	**L**	I	23
18	32	P	**L**	C	S	L	Y	L	I	**A**	V	22
19	119	A	**M**	A	F	D	R	Y	V	**A**	I	22
20	237	K	**A**	F	G	T	C	V	S	**H**	V	22
21	275	V	**I**	L	A	N	I	Y	L	**L**	V	22
22	85	A	**I**	F	W	F	N	S	T	**T**	I	21
23	139	T	**L**	P	R	V	T	K	I	**G**	V	21
24	202	L	**I**	V	I	I	S	A	I	**G**	L	21
25	13	Y	**F**	I	L	I	G	L	P	**G**	L	20
26	16	L	**I**	G	L	P	G	L	E	**E**	A	20
27	29	L	**A**	F	P	L	C	S	L	**Y**	L	20
28	142	R	**V**	T	K	I	G	V	A	**A**	V	20
29	148	V	**A**	A	V	V	R	G	A	**A**	L	20
30	167	Q	**L**	P	F	C	R	S	N	**I**	L	20
31	180	Y	**C**	L	H	Q	D	V	M	**K**	L	20
32	222	L	**I**	L	K	T	V	L	G	**L**	T	20
33	240	G	**T**	C	V	S	H	V	C	**A**	V	20
34	248	A	**V**	F	I	F	Y	V	P	**F**	I	20
35	250	F	**I**	F	Y	V	P	F	I	**G**	L	20
36	271	S	**P**	L	P	V	I	L	A	**N**	I	20
37	279	N	**I**	Y	L	L	V	P	P	**V**	L	20
38	304	I	**L**	R	L	F	H	V	A	**T**	H	20
39	10	S	**A**	T	Y	F	I	L	I	**G**	L	19
40	15	I	**L**	I	G	L	P	G	L	**E**	E	19
41	27	F	**W**	L	A	F	P	L	C	**S**	L	19
42	35	S	**L**	Y	L	I	A	V	L	**G**	N	19
43	37	Y	**L**	I	A	V	L	G	N	**L**	T	19
44	44	N	**L**	T	I	I	Y	I	V	**R**	T	19
45	64	F	**L**	C	M	L	S	G	I	**D**	I	19
46	83	M	**L**	A	I	F	W	F	N	**S**	T	19
47	159	A	**P**	L	P	V	F	I	K	**Q**	L	19
48	189	L	**A**	C	D	D	I	R	V	**N**	V	19
49	207	S	**A**	I	G	L	D	S	L	**L**	I	19
50	253	Y	**V**	P	F	I	G	L	S	**M**	V	19

HLA-A*0201 decamers(SEQ ID NOS 2154-2253, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
51	276	I	**L**	A	N	I	Y	L	L	**V**	P	19
52	281	Y	**L**	L	V	P	P	V	L	**N**	P	19
53	283	L	**V**	P	P	V	L	N	P	**I**	V	19
54	286	P	**V**	L	N	P	I	V	Y	**G**	V	19
55	33	L	**C**	S	L	Y	L	I	A	**V**	L	18
56	36	L	**Y**	L	I	A	V	L	G	**N**	L	18
57	39	I	**A**	V	L	G	N	L	T	**I**	I	18
58	42	L	**G**	N	L	T	I	I	Y	**I**	V	18
59	66	C	**M**	L	S	G	I	D	I	**L**	I	18
60	111	G	**M**	E	S	T	V	L	L	**A**	M	18
61	128	I	**C**	H	P	L	R	H	A	**T**	V	18
62	134	H	**A**	T	V	L	T	L	P	**R**	V	18
63	154	G	**A**	A	L	M	A	P	L	**P**	V	18
64	157	L	**M**	A	P	L	P	V	F	**I**	K	18
65	190	A	**C**	D	D	I	R	V	N	**V**	V	18
66	229	G	**L**	T	R	E	A	Q	A	**K**	A	18
67	245	H	**V**	C	A	V	F	I	F	**Y**	V	18
68	274	P	**V**	I	L	A	N	I	Y	**L**	L	18
69	278	A	**N**	I	Y	L	L	V	P	**P**	V	18
70	291	I	**V**	Y	G	V	K	T	K	**E**	I	18
71	298	K	**E**	I	R	Q	R	I	L	**R**	L	18
72	48	I	**Y**	I	V	R	T	E	H	**S**	L	17
73	65	L	**C**	M	L	S	G	I	D	**I**	L	17
74	67	M	**L**	S	G	I	D	I	L	**I**	S	17
75	74	L	**I**	S	T	S	S	M	P	**K**	M	17
76	91	S	**T**	T	I	Q	F	D	A	**C**	L	17
77	94	I	**Q**	F	D	A	C	L	L	**Q**	I	17
78	188	K	**L**	A	C	D	D	I	R	**V**	N	17
79	197	N	**V**	V	Y	G	L	I	V	**I**	I	17
80	200	Y	**G**	L	I	V	I	I	S	**A**	I	17
81	218	F	**S**	Y	L	L	I	L	K	**T**	V	17
82	227	V	**L**	G	L	T	R	E	A	**Q**	A	17
83	303	R	**I**	L	R	L	F	H	V	**A**	T	17
84	21	G	**L**	E	E	A	Q	F	W	**L**	A	16
85	92	T	**T**	I	Q	F	D	A	C	**L**	L	16
86	97	D	**A**	C	L	L	Q	I	F	**A**	I	16
87	127	A	**I**	C	H	P	L	R	H	**A**	T	16
88	143	V	**T**	K	I	G	V	A	A	**V**	V	16
89	195	R	**V**	N	V	V	Y	G	L	**I**	V	16
90	220	Y	**L**	L	I	L	K	T	V	**L**	G	16
91	296	K	**T**	K	E	I	R	Q	R	**I**	L	16
92	18	G	**L**	P	G	L	E	E	A	**Q**	F	15
93	30	A	**F**	P	L	C	S	L	Y	**L**	I	15
94	126	V	**A**	I	C	H	P	L	R	**H**	A	15
95	145	K	**I**	G	V	A	A	V	V	**R**	G	15
96	173	S	**N**	I	L	S	H	S	Y	**C**	L	15
97	201	G	**L**	I	V	I	I	S	A	**I**	G	15
98	208	A	**I**	G	L	D	S	L	L	**I**	S	15
99	210	G	**L**	D	S	L	L	I	S	**F**	S	15
100	267	K	**R**	R	D	S	P	L	P	**V**	I	15

HLA-A*0201 decamers(SEQ ID NOS 2154-2253, respectively in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score

HLA-A*0203 decamers(SEQ ID NOS 2254-2301, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	141	P	R	**V**	T	K	I	G	V	**A**	A	19
2	147	G	V	**A**	A	V	V	R	G	**A**	A	19
3	112	M	E	**S**	T	V	L	L	A	**M**	A	18
4	227	V	L	**G**	L	T	R	E	A	**Q**	A	18
5	229	G	L	**T**	R	E	A	Q	A	**K**	A	18
6	142	R	V	**T**	K	I	G	V	A	**A**	V	17
7	148	V	A	**A**	V	V	R	G	A	**A**	L	17
8	2	V	D	**P**	N	G	N	E	S	**S**	A	10
9	16	L	I	**G**	L	P	G	L	E	**E**	A	10
10	21	G	L	**E**	E	A	Q	F	W	**L**	A	10
11	31	F	P	**L**	C	S	L	Y	L	**I**	A	10
12	76	S	T	**S**	S	M	P	K	M	**L**	A	10
13	89	F	N	**S**	T	T	I	Q	F	**D**	A	10
14	96	F	D	**A**	C	L	L	Q	I	**F**	A	10
15	110	S	G	**M**	E	S	T	V	L	**L**	A	10
16	118	L	A	**M**	A	F	D	R	Y	**V**	A	10
17	126	V	A	**I**	C	H	P	L	R	**H**	A	10
18	140	L	P	**R**	V	T	K	I	G	**V**	A	10
19	146	I	G	**V**	A	A	V	V	R	**G**	A	10
20	150	A	V	**V**	R	G	A	A	L	**M**	A	10
21	181	C	L	**H**	Q	D	V	M	K	**L**	A	10
22	199	V	Y	**G**	L	I	V	I	I	**S**	A	10
23	225	K	T	**V**	L	G	L	T	R	**E**	A	10
24	239	F	G	**T**	C	V	S	H	V	**C**	A	10
25	269	R	D	**S**	P	L	P	V	I	**L**	A	10
26	302	Q	R	**I**	L	R	L	F	H	**V**	A	10
27	305	L	R	**L**	F	H	V	A	T	**H**	A	10
28	3	D	P	**N**	G	N	E	S	S	**A**	T	9
29	17	I	G	**L**	P	G	L	E	E	**A**	Q	9
30	22	L	E	**E**	A	Q	F	W	L	**A**	F	9
31	32	P	L	**C**	S	L	Y	L	I	**A**	V	9
32	77	T	S	**S**	M	P	K	M	L	**A**	I	9
33	90	N	S	**T**	T	I	Q	F	D	**A**	C	9
34	97	D	A	**C**	L	L	Q	I	F	**A**	I	9
35	111	G	M	**E**	S	T	V	L	L	**A**	M	9
36	113	E	S	**T**	V	L	L	A	M	**A**	F	9
37	119	A	M	**A**	F	D	R	Y	V	**A**	I	9
38	127	A	I	**C**	H	P	L	R	H	**A**	T	9
39	151	V	V	**R**	G	A	A	L	M	**A**	P	9
40	182	L	H	**Q**	D	V	M	K	L	**A**	C	9
41	200	Y	G	**L**	I	V	I	I	S	**A**	I	9
42	226	T	V	**L**	G	L	T	R	E	**A**	Q	9
43	228	L	G	**L**	T	R	E	A	Q	**A**	K	9

HLA-A*0203 decamers(SEQ ID NOS 2254-2301, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
44	230	L	T	**R**	E	A	Q	A	K	**A**	F	9
45	240	G	T	**C**	V	S	H	V	C	**A**	V	9
46	270	D	S	**P**	L	P	V	I	L	**A**	N	9
47	303	R	I	**L**	R	L	F	H	V	**A**	T	9
48	306	R	L	**F**	H	V	A	T	H	**A**	S	9

HLA-A26 decamers(SEQ ID NOS 2302-2366, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	299	E	I	R	Q	R	I	L	R	L	F	31
2	193	D	I	R	V	N	V	V	Y	G	L	29
3	250	F	I	F	Y	V	P	F	I	G	L	25
4	256	F	I	G	L	S	M	V	H	R	F	25
5	74	L	I	S	T	S	S	M	P	K	M	24
6	274	P	V	I	L	A	N	I	Y	L	L	24
7	18	G	L	P	G	L	E	E	A	Q	F	23
8	116	V	L	L	A	M	A	F	D	R	Y	23
9	205	I	I	S	A	I	G	L	D	S	L	23
10	221	L	L	I	L	K	T	V	L	G	L	23
11	230	L	T	R	E	A	Q	A	K	A	F	23
12	13	Y	F	I	L	I	G	L	P	G	L	22
13	40	A	V	L	G	N	L	T	I	I	Y	22
14	56	S	L	H	E	P	M	Y	I	F	L	22
15	95	Q	F	D	A	C	L	L	Q	I	F	22
16	215	L	I	S	F	S	Y	L	L	I	L	22
17	92	T	T	I	Q	F	D	A	C	L	L	21
18	100	L	L	Q	I	F	A	I	H	S	L	21
19	103	I	F	A	I	H	S	L	S	G	M	21
20	296	K	T	K	E	I	R	Q	R	I	L	21
21	28	W	L	A	F	P	L	C	S	L	Y	20
22	131	P	L	R	H	A	T	V	L	T	L	20
23	59	E	P	M	Y	I	F	L	C	M	L	19
24	91	S	T	T	I	Q	F	D	A	C	L	19
25	202	L	I	V	I	I	S	A	I	G	L	19
26	212	D	S	L	L	I	S	F	S	Y	L	19
27	272	P	L	P	V	I	L	A	N	I	Y	19
28	279	N	I	Y	L	L	V	P	P	V	L	19
29	52	R	T	E	H	S	L	H	E	P	M	18
30	62	Y	I	F	L	C	M	L	S	G	I	18
31	72	D	I	L	I	S	T	S	S	M	P	18
32	108	S	L	S	G	M	E	S	T	V	L	18
33	113	E	S	T	V	L	L	A	M	A	F	18
34	151	V	V	R	G	A	A	L	M	A	P	18
35	78	S	S	M	P	K	M	L	A	I	F	17
36	142	R	V	T	K	I	G	V	A	A	V	17
37	162	P	V	F	I	K	Q	L	P	F	C	17
38	164	F	I	K	Q	L	P	F	C	R	S	17

HLA-A26 decamers(SEQ ID NOS 2302-2366, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
39	167	Q	L	P	F	C	R	S	N	I	L	17
40	185	D	V	M	K	L	A	C	D	D	I	17
41	248	A	V	F	I	F	Y	V	P	F	I	17
42	253	Y	V	P	F	I	G	L	S	M	V	17
43	45	L	T	I	I	Y	I	V	R	T	E	16
44	145	K	I	G	V	A	A	V	V	R	G	16
45	198	V	V	Y	G	L	I	V	I	I	S	16
46	203	I	V	I	I	S	A	I	G	L	D	16
47	209	I	G	L	D	S	L	L	I	S	F	16
48	213	S	L	L	I	S	F	S	Y	L	L	16
49	255	P	F	I	G	L	S	M	V	H	R	16
50	264	R	F	S	K	R	R	D	S	P	L	16
51	294	G	V	K	T	K	E	I	R	Q	R	16
52	16	L	I	G	L	P	G	L	E	E	A	15
53	80	M	P	K	M	L	A	I	F	W	F	15
54	114	S	T	V	L	L	A	M	A	F	D	15
55	155	A	A	L	M	A	P	L	P	V	F	15
56	159	A	P	L	P	V	F	I	K	Q	L	15
57	174	N	I	L	S	H	S	Y	C	L	H	15
58	197	N	V	V	Y	G	L	I	V	I	I	15
59	210	G	L	D	S	L	L	I	S	F	S	15
60	214	L	L	I	S	F	S	Y	L	L	I	15
61	222	L	I	L	K	T	V	L	G	L	T	15
62	240	G	T	C	V	S	H	V	C	A	V	15
63	247	C	A	V	F	I	F	Y	V	P	F	15
64	286	P	V	L	N	P	I	V	Y	G	V	15
65	298	K	E	I	R	Q	R	I	L	R	L	15

HLA-A3 decamers(SEQ ID NOS 2367-2432, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	136	T	**V**	L	T	L	P	R	V	**T**	K	31
2	287	V	**L**	N	P	I	V	Y	G	**V**	K	28
3	223	I	**L**	K	T	V	L	G	L	**T**	R	27
4	304	I	**L**	R	L	F	H	V	A	**T**	H	27
5	73	I	**L**	I	S	T	S	S	M	**P**	K	26
6	15	I	**L**	I	G	L	P	G	L	**E**	E	23
7	40	A	**V**	L	G	N	L	T	I	**I**	Y	23
8	150	A	**V**	V	R	G	A	A	L	**M**	A	23
9	258	G	**L**	S	M	V	H	R	F	**S**	K	23
10	18	G	**L**	P	G	L	E	E	A	**Q**	F	22
11	303	R	**I**	L	R	L	F	H	V	**A**	T	22
12	276	I	**L**	A	N	I	Y	L	L	**V**	P	21
13	28	W	**L**	A	F	P	L	C	S	**L**	Y	20
14	115	T	**V**	L	L	A	M	A	F	**D**	R	20
15	116	V	**L**	L	A	M	A	F	D	**R**	Y	20
16	125	Y	**V**	A	I	C	H	P	L	**R**	H	20
17	131	P	**L**	R	H	A	T	V	L	**T**	L	20
18	144	T	**K**	I	G	V	A	A	V	**V**	R	20

HLA-A3 decamers(SEQ ID NOS 2367-2432, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
19	156	A	**L**	M	A	P	L	P	V	**F**	I	20
20	195	R	**V**	N	V	V	Y	G	L	**I**	V	20
21	35	S	**L**	Y	L	I	A	V	L	**G**	N	19
22	272	P	**L**	P	V	I	L	A	N	**I**	Y	19
23	37	Y	**L**	I	A	V	L	G	N	**L**	T	18
24	49	Y	**I**	V	R	T	E	H	S	**L**	H	18
25	50	I	**V**	R	T	E	H	S	L	**H**	E	18
26	108	S	**L**	S	G	M	E	S	T	**V**	L	18
27	142	R	**V**	T	K	I	G	V	A	**A**	V	18
28	188	K	**L**	A	C	D	D	I	R	**V**	N	18
29	279	N	**I**	Y	L	L	V	P	P	**V**	L	18
30	291	I	**V**	Y	G	V	K	T	K	**E**	I	18
31	294	G	**V**	K	T	K	E	I	R	**Q**	R	18
32	46	T	**I**	I	Y	I	V	R	T	**E**	H	17
33	102	Q	**I**	F	A	I	H	S	L	**S**	G	17
34	151	V	**V**	R	G	A	A	L	M	**A**	P	17
35	179	S	**Y**	C	L	H	Q	D	V	**M**	K	17
36	203	I	**V**	I	I	S	A	I	G	**L**	D	17
37	204	V	**I**	I	S	A	I	G	L	**D**	S	17
38	220	Y	**L**	L	I	L	K	T	V	**L**	G	17
39	221	L	**L**	I	L	K	T	V	L	**G**	L	17
40	227	V	**L**	G	L	T	R	E	A	**Q**	A	17
41	242	C	**V**	S	H	V	C	A	V	**F**	I	17
42	289	N	**P**	I	V	Y	G	V	K	**T**	K	17
43	38	L	**I**	A	V	L	G	N	L	**T**	I	16
44	85	A	**I**	F	W	F	N	S	T	**T**	I	16
45	147	G	**V**	A	A	V	V	R	G	**A**	A	16
46	198	V	**V**	Y	G	L	I	V	I	**I**	S	16
47	201	G	**L**	I	V	I	I	S	A	**I**	G	16
48	214	L	**L**	I	S	F	S	Y	L	**L**	I	16
49	226	T	**V**	L	G	L	T	R	E	**A**	Q	16
50	228	L	**G**	L	T	R	E	A	Q	**A**	K	16
51	229	G	**L**	T	R	E	A	Q	A	**K**	A	16
52	1	M	**V**	D	P	N	G	N	E	**S**	S	15
53	44	N	**L**	T	I	I	Y	I	V	**R**	T	15
54	47	I	**I**	Y	I	V	R	T	E	**H**	S	15
55	67	M	**L**	S	G	I	D	I	L	**I**	S	15
56	72	D	**I**	L	I	S	T	S	S	**M**	P	15
57	99	C	**L**	L	Q	I	F	A	I	**H**	S	15
58	105	A	**I**	H	S	L	S	G	M	**E**	S	15
59	145	K	**I**	G	V	A	A	V	V	**R**	G	15
60	175	I	**L**	S	H	S	Y	C	L	**H**	Q	15
61	191	C	**D**	D	I	R	V	N	V	**V**	Y	15
62	208	A	**I**	G	L	D	S	L	L	**I**	S	15
63	275	V	**I**	L	A	N	I	Y	L	**L**	V	15
64	281	Y	**L**	L	V	P	P	V	L	**N**	P	15
65	299	E	**I**	R	Q	R	I	L	R	**L**	F	15
66	306	R	**L**	F	H	V	A	T	H	**A**	S	15

HLA-B*0702 decamers(SEQ ID

NOS 2433-2492, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	159	A	**P**	L	P	V	F	I	K	**Q**	L	23
2	59	E	**P**	M	Y	I	F	L	C	**M**	L	22
3	273	L	**P**	V	I	L	A	N	I	**Y**	L	20
4	3	D	**P**	N	G	N	E	S	S	**A**	T	19
5	130	H	**P**	L	R	H	A	T	V	**L**	T	19
6	140	L	**P**	R	V	T	K	I	G	**V**	A	19
7	161	L	**P**	V	F	I	K	Q	L	**P**	F	19
8	31	F	**P**	L	C	S	L	Y	L	**I**	A	18
9	271	S	**P**	L	P	V	I	L	A	**N**	I	18
10	80	M	**P**	K	M	L	A	I	F	**W**	F	16
11	108	S	**L**	S	G	M	E	S	T	**V**	L	16
12	131	P	**L**	R	H	A	T	V	L	**T**	L	15
13	264	R	**F**	S	K	R	R	D	S	**P**	L	15
14	33	L	**C**	S	L	Y	L	I	A	**V**	L	14
15	109	L	**S**	G	M	E	S	T	V	**L**	L	14
16	152	V	**R**	G	A	A	L	M	A	**P**	L	14
17	205	I	**I**	S	A	I	G	L	D	**S**	L	14
18	215	L	**I**	S	F	S	Y	L	L	**I**	L	14
19	268	R	**R**	D	S	P	L	P	V	**I**	L	14
20	29	L	**A**	F	P	L	C	S	L	**Y**	L	13
21	148	V	**A**	A	V	V	R	G	A	**A**	L	13
22	156	A	**L**	M	A	P	L	P	V	**F**	I	13
23	193	D	**I**	R	V	N	V	V	Y	**G**	L	13
24	221	L	**L**	I	L	K	T	V	L	**G**	L	13
25	298	K	**E**	I	R	Q	R	I	L	**R**	L	13
26	7	N	**E**	S	S	A	T	Y	F	**I**	L	12
27	19	L	**P**	G	L	E	E	A	Q	**F**	W	12
28	24	E	**A**	Q	F	W	L	A	F	**P**	L	12
29	119	A	**M**	A	F	D	R	Y	V	**A**	I	12
30	129	C	**H**	P	L	R	H	A	T	**V**	L	12
31	206	I	**S**	A	I	G	L	D	S	**L**	L	12
32	219	S	**Y**	L	L	I	L	K	T	**V**	L	12
33	279	N	**I**	Y	L	L	V	P	P	**V**	L	12
34	285	P	**P**	V	L	N	P	I	V	**Y**	G	12
35	8	E	**S**	S	A	T	Y	F	I	**L**	I	11
36	13	Y	**F**	I	L	I	G	L	P	**G**	L	11
37	27	F	**W**	L	A	F	P	L	C	**S**	L	11
38	48	I	**Y**	I	V	R	T	E	H	**S**	L	11
39	56	S	**L**	H	E	P	M	Y	I	**F**	L	11
40	65	L	**C**	M	L	S	G	I	D	**I**	L	11
41	75	I	**S**	T	S	S	M	P	K	**M**	L	11
42	77	T	**S**	S	M	P	K	M	L	**A**	I	11
43	91	S	**T**	T	I	Q	F	D	A	**C**	L	11
44	123	D	**R**	Y	V	A	I	C	H	**P**	L	11
45	142	R	**V**	T	K	I	G	V	A	**A**	V	11
46	180	Y	**C**	L	H	Q	D	V	M	**K**	L	11
47	190	A	**C**	D	D	I	R	V	N	**V**	V	11
48	212	D	**S**	L	L	I	S	F	S	**Y**	L	11
49	234	A	**Q**	A	K	A	F	G	T	**C**	V	11
50	242	C	**V**	S	H	V	C	A	V	**F**	I	11
51	248	A	**V**	F	I	F	Y	V	P	**F**	I	11

HLA-B*0702 decamers(SEQ ID NOS 2433-2492, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
52	250	F	**I**	F	Y	V	P	F	I	**G**	L	11
53	254	V	**P**	F	I	G	L	S	M	**V**	H	11
54	266	S	**K**	R	R	D	S	P	L	**P**	V	11
55	267	K	**R**	R	D	S	P	L	P	**V**	I	11
56	269	R	**D**	S	P	L	P	V	I	**L**	A	11
57	278	A	**N**	I	Y	L	L	V	P	**P**	V	11
58	284	V	**P**	P	V	L	N	P	I	**V**	Y	11
59	289	N	**P**	I	V	Y	G	V	K	**T**	K	11
60	296	K	**T**	K	E	I	R	Q	R	**I**	L	11

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Please replace Table XXVIII, beginning at page 205, line 1, with the following rewritten Table XXVIII:

--Table XXVIII:

HLA Class II Epitopes (sample 15-mer length)

(SEQ ID NOS 2493-2595, respectively in order of appearance)

HLA-DRB1*0101 15-mers

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	200	**Y**	G	L	**I**	V	**I**	I	S	**A**	I	G	L	D	S	L	36
2	68	**L**	S	G	**I**	D	**I**	L	I	**S**	T	S	S	M	P	K	34
3	62	**Y**	I	F	**L**	C	**M**	L	S	**G**	I	D	I	L	I	S	33
4	103	**I**	F	A	**I**	H	**S**	L	S	**G**	M	E	S	T	V	L	32
5	45	**L**	T	I	**I**	Y	**I**	V	R	**T**	E	H	S	L	H	E	31
6	193	**D**	I	R	**V**	N	**V**	V	Y	**G**	L	I	V	I	I	S	31
7	277	**L**	A	N	**I**	Y	**L**	L	V	**P**	P	V	L	N	P	I	31
8	97	**D**	A	C	**L**	L	**Q**	I	F	**A**	I	H	S	L	S	G	30
9	106	**I**	H	S	**L**	S	**G**	M	E	**S**	T	V	L	L	A	M	30
10	240	**G**	T	C	**V**	S	**H**	V	C	**A**	V	F	I	F	Y	V	30
11	10	**S**	A	T	**Y**	F	**I**	L	I	**G**	L	P	G	L	E	E	29
12	289	**N**	P	I	**V**	Y	**G**	V	K	**T**	K	E	I	R	Q	R	29
13	11	**A**	T	Y	**F**	I	**L**	I	G	**L**	P	G	L	E	E	A	28
14	250	**F**	I	F	**Y**	V	**P**	F	I	**G**	L	S	M	V	H	R	27
15	140	**L**	P	R	**V**	T	**K**	I	G	**V**	A	A	V	V	R	G	26
16	183	**H**	Q	D	**V**	M	**K**	L	A	**C**	D	D	I	R	V	N	26
17	217	**S**	F	S	**Y**	L	**L**	I	L	**K**	T	V	L	G	L	T	26
18	16	**L**	I	G	**L**	P	**G**	L	E	**E**	A	Q	F	W	L	A	25
19	24	**E**	A	Q	**F**	W	**L**	A	F	**P**	L	C	S	L	Y	L	25
20	36	**L**	Y	L	**I**	A	**V**	L	G	**N**	L	T	I	I	Y	I	25
21	70	**G**	I	D	**I**	L	**I**	S	T	**S**	S	M	P	K	M	L	25
22	111	**G**	M	E	**S**	T	**V**	L	L	**A**	M	A	F	D	R	Y	25
23	148	**V**	A	A	**V**	V	**R**	G	A	**A**	L	M	A	P	L	P	25
24	162	**P**	V	F	**I**	K	**Q**	L	P	**F**	C	R	S	N	I	L	25
25	197	**N**	V	V	**Y**	G	**L**	I	V	**I**	I	S	A	I	G	L	25
26	211	**L**	D	S	**L**	L	**I**	S	F	**S**	Y	L	L	I	L	K	25

HLA-DRB1*0101 15-mers

Pos		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
27	218	**F**	S	Y	**L**	L	**I**	L	K	**T**	V	L	G	L	T	R	25
28	13	**Y**	F	I	**L**	I	**G**	L	P	**G**	L	E	E	A	Q	F	24
29	30	**A**	F	P	**L**	C	**S**	L	Y	**L**	I	A	V	L	G	N	24
30	39	I	A	V	**L**	G	**N**	L	T	**I**	I	Y	I	V	R	T	24
31	77	**T**	S	S	**M**	P	**K**	M	L	**A**	I	F	W	F	N	S	24
32	85	**A**	I	F	**W**	F	**N**	S	T	**T**	I	Q	F	D	A	C	24
33	137	**V**	L	T	**L**	P	**R**	V	T	**K**	I	G	V	A	A	V	24
34	151	**V**	V	R	**G**	A	**A**	L	M	**A**	P	L	P	V	F	I	24
35	161	**L**	P	V	**F**	I	**K**	Q	L	**P**	F	C	R	S	N	I	24
36	196	**V**	N	V	**V**	Y	**G**	L	I	**V**	I	I	S	A	I	G	24
37	202	**L**	I	V	**I**	I	**S**	A	I	**G**	L	D	S	L	L	I	24
38	208	**A**	I	G	**L**	D	**S**	L	L	**I**	S	F	S	Y	L	L	24
39	248	**A**	V	F	**I**	F	**Y**	V	P	**F**	I	G	L	S	M	V	24
40	251	**I**	F	Y	**V**	P	**F**	I	G	**L**	S	M	V	H	R	F	24
41	83	**M**	L	A	**I**	F	**W**	F	N	**S**	T	T	I	Q	F	D	23
42	101	**L**	Q	I	**F**	A	**I**	H	S	**L**	S	G	M	E	S	T	23
43	165	I	K	Q	**L**	P	**F**	C	R	**S**	N	I	L	S	H	S	23
44	203	**I**	V	I	**I**	S	**A**	I	G	**L**	D	S	L	L	I	S	23
45	221	**L**	L	I	**L**	K	**T**	V	L	**G**	L	T	R	E	A	Q	23
46	278	**A**	N	I	**Y**	L	**L**	V	P	**P**	V	L	N	P	I	V	23
47	27	**F**	W	L	**A**	F	**P**	L	C	**S**	L	Y	L	I	A	V	22
48	35	**S**	L	Y	**L**	I	**A**	V	L	**G**	N	L	T	I	I	Y	22
49	61	**M**	Y	I	**F**	L	**C**	M	L	**S**	G	I	D	I	L	I	22
50	65	**L**	C	M	**L**	S	**G**	I	D	**I**	L	I	S	T	S	S	22
51	80	**M**	P	K	**M**	L	**A**	I	F	**W**	F	N	S	T	T	I	22
52	145	**K**	I	G	**V**	A	**A**	V	V	**R**	G	A	A	L	M	A	22
53	146	**I**	G	V	**A**	A	**V**	V	R	**G**	A	A	L	M	A	P	22
54	154	**G**	A	A	**L**	M	**A**	P	L	**P**	V	F	I	K	Q	L	22
55	205	**I**	I	S	**A**	I	**G**	L	D	**S**	L	L	I	S	F	S	22
56	243	**V**	S	H	**V**	C	**A**	V	F	**I**	F	Y	V	P	F	I	22
57	270	**D**	S	P	**L**	P	**V**	I	L	**A**	N	I	Y	L	L	V	22
58	274	**P**	V	I	**L**	A	**N**	I	Y	**L**	L	V	P	P	V	L	22
59	281	**Y**	L	L	**V**	P	**P**	V	L	**N**	P	I	V	Y	G	V	22
60	34	**C**	S	L	**Y**	L	**I**	A	V	**L**	G	N	L	T	I	I	21
61	69	**S**	G	I	**D**	I	**L**	I	S	**T**	S	S	M	P	K	M	21
62	152	**V**	R	G	**A**	A	**L**	M	A	**P**	L	P	V	F	I	K	21
63	299	**E**	I	R	**Q**	R	**I**	L	R	**L**	F	H	V	A	T	H	21
64	100	**L**	L	Q	**I**	F	**A**	I	H	**S**	L	S	G	M	E	S	20
65	135	**A**	T	V	**L**	T	**L**	P	R	**V**	T	K	I	G	V	A	20
66	141	**P**	R	V	**T**	K	**I**	G	V	**A**	A	V	V	R	G	A	20
67	191	**C**	D	D	**I**	R	**V**	N	V	**V**	Y	G	L	I	V	I	20
68	199	**V**	Y	G	**L**	I	**V**	I	I	**S**	A	I	G	L	D	S	20
69	262	**V**	H	R	**F**	S	**K**	R	R	**D**	S	P	L	P	V	I	20
70	271	**S**	P	L	**P**	V	**I**	L	A	**N**	I	Y	L	L	V	P	20
71	28	**W**	L	A	**F**	P	**L**	C	S	**L**	Y	L	I	A	V	L	19
72	58	**H**	E	P	**M**	Y	**I**	F	L	**C**	M	L	S	G	I	D	19
73	59	**E**	P	M	**Y**	I	**F**	L	C	**M**	L	S	G	I	D	I	19
74	60	**P**	M	Y	**I**	F	**L**	C	M	**L**	S	G	I	D	I	L	19
75	98	**A**	C	L	**L**	Q	**I**	F	A	**I**	H	S	L	S	G	M	19
76	215	**L**	I	S	**F**	S	**Y**	L	L	**I**	L	K	T	V	L	G	19
77	219	**S**	Y	L	**L**	I	**L**	K	T	**V**	L	G	L	T	R	E	19

HLA-DRB1*0101 15-mers

Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score
78 228	L G L T R E A Q A K A F G T C	19
79 232	R E A Q A K A F G T C V S H V	19
80 246	V C A V F I F Y V P F I G L S	19
81 297	T K E I R Q R I L R L F H V A	19
82 3	D P N G N E S S A T Y F I L I	18
83 14	F I L I G L P G L E E A Q F W	18
84 25	A Q F W L A F P L C S L Y L I	18
85 42	L G N L T I I Y I V R T E H S	18
86 46	T I I Y I V R T E H S L H E P	18
87 78	S S M P K M L A I F W F N S T	18
88 84	L A I F W F N S T T I Q F D A	18
89 89	F N S T T I Q F D A C L L Q I	18
90 93	T I Q F D A C L L Q I F A I H	18
91 115	T V L L A M A F D R Y V A I C	18
92 119	A M A F D R Y V A I C H P L R	18
93 127	A I C H P L R H A T V L T L P	18
94 129	C H P L R H A T V L T L P R V	18
95 147	G V A A V V R G A A L M A P L	18
96 149	A A V V R G A A L M A P L P V	18
97 216	I S F S Y L L I L K T V L G L	18
98 227	V L G L T R E A Q A K A F G T	18
99 249	V F I F Y V P F I G L S M V H	18
100 253	Y V P F I G L S M V H R F S K	18
101 284	V P P V L N P I V Y G V K T K	18
102 286	P V L N P I V Y G V K T K E I	18
103 303	R I L R L F H V A T H A S E P	18

HLA-DRB1*0301 (DR17) 15-mers

(SEQ ID NOS 2596-2671, respectively in order of appearance)

Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score
1 16	L I G L P G L E E A Q F W L A	26
2 206	I S A I G L D S L L I S F S Y	23
3 91	S T T I Q F D A C L L Q I F A	22
4 117	L L A M A F D R Y V A I C H P	22
5 38	L I A V L G N L T I I Y I V R	21
6 179	S Y C L H Q D V M K L A C D D	21
7 211	L D S L L I S F S Y L L I L K	21
8 219	S Y L L I L K T V L G L T R E	21
9 272	P L P V I L A N I Y L L V P P	21
10 26	Q F W L A F P L C S L Y L I A	20
11 114	S T V L L A M A F D R Y V A I	20
12 129	C H P L R H A T V L T L P R V	20
13 134	H A T V L T L P R V T K I G V	20
14 186	V M K L A C D D I R V N V V Y	20
15 200	Y G L I V I I S A I G L D S L	20
16 270	D S P L P V I L A N I Y L L V	20
17 297	T K E I R Q R I L R L F H V A	20
18 11	A T Y F I L I G L P G L E E A	19
19 54	E H S L H E P M Y I F L C M L	19

HLA-DRB1*0301 (DR17) 15-mers

(SEQ ID NOS 2596-2671, respectively in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
20 106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	19
21 165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	19
22 191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	19
23 203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	19
24 213	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	V	19
25 224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	19
26 227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	19
27 248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	19
28 254	V	P	F	I	G	L	S	M	V	H	R	F	S	K	R	19
29 277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	19
30 36	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	I	18
31 93	T	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	18
32 98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	18
33 125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	18
34 158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	18
35 187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
36 217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	18
37 225	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	F	18
38 281	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	V	18
39 288	L	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	18
40 18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	17
41 44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	17
42 145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	17
43 159	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	S	17
44 256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	17
45 259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	17
46 137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	16
47 262	V	H	R	F	S	K	R	R	D	S	P	L	P	V	I	16
48 294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	16
49 46	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	15
50 51	V	R	T	E	H	S	L	H	E	P	M	Y	I	F	L	15
51 172	R	S	N	I	L	S	H	S	Y	C	L	H	Q	D	V	15
52 189	L	A	C	D	D	I	R	V	N	V	V	Y	G	L	I	15
53 212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	15
54 218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	15
55 271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	15
56 279	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	15
57 12	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	14
58 35	S	L	Y	L	I	A	V	L	G	N	L	T	I	I	Y	14
59 64	F	L	C	M	L	S	G	I	D	I	L	I	S	T	S	14
60 140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	14
61 273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
62 301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	14
63 13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	13
64 47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	13
65 71	I	D	I	L	I	S	T	S	S	M	P	K	M	L	A	13
66 80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	13
67 109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	13
68 113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	13

HLA-DRB1*0301 (DR17) 15-mers

(SEQ ID NOS 2596-2671, respectively in order of appearance)

Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score
69 135	**A** T V **L** T **L** P R **V** T K I G V A	13
70 195	**R** V N **V** V **Y** G L **I** V I I S A I	13
71 202	**L** I V **I** I **S** A I **G** L D S L L I	13
72 220	**Y** L L **I** L **K** T V **L** G L T R E A	13
73 221	**L** L I **L** K **T** V L **G** L T R E A Q	13
74 264	**R** F S **K** R **R** D S **P** L P V I L A	13
75 280	**I** Y L **L** V **P** P V **L** N P I V Y G	13
76 302	**Q** R I **L** R **L** F H **V** A T H A S E	13

HLA-DRB1*0401 (DR4Dw4) 15-mers

(SEQ ID NOS 2672-2805, respectively in order of appearance)

Pos	1 2 3 4 5 6 7 8 9 0 1 2 3 4 5	score
1 36	**L** Y L **I** A **V** **L** G **N** L T I I Y I	26
2 45	**L** T I **I** Y **I** **V** R **T** E H S L H E	26
3 68	**L** S G **I** D **I** **L** I **S** T S S M P K	26
4 83	**M** L A **I** F **W** **F** N **S** T T I Q F D	26
5 134	**H** A T **V** L **T** **L** P **R** V T K I G V	26
6 145	**K** I G **V** A **A** **V** V **R** G A A L M A	26
7 224	**L** K T **V** L **G** **L** T **R** E A Q A K A	26
8 227	**V** L G **L** T **R** **E** A **Q** A K A F G T	26
9 256	**F** I G **L** S **M** **V** H **R** F S K R R D	26
10 281	**Y** L L **V** P **P** **V** L **N** P I V Y G V	26
11 289	**N** P I **V** Y **G** **V** K **T** K E I R Q R	26
12 301	**R** Q R **I** L **R** **L** F **H** V A T H A S	26
13 11	**A** T Y **F** I **L** **I** G **L** P G L E E A	22
14 24	**E** A Q **F** W **L** **A** F **P** L C S L Y L	22
15 25	**A** Q F **W** L **A** **F** P **L** C S L Y L I	22
16 34	**C** S L **Y** L **I** **A** V **L** G N L T I I	22
17 84	**L** A I **F** W **F** **N** S **T** T I Q F D A	22
18 122	**F** D R **Y** V **A** **I** C **H** P L R H A T	22
19 197	**N** V V **Y** G **L** **I** V **I** I S A I G L	22
20 215	**L** I S **F** S **Y** **L** L **I** L K T V L G	22
21 217	**S** F S **Y** L **L** **I** L **K** T V L G L T	22
22 250	**F** I F **Y** V **P** **F** I **G** L S M V H R	22
23 278	**A** N I **Y** L **L** **V** P **P** V L N P I V	22
24 19	**L** P G L E **E** **A** Q **F** W L A F P L	20
25 30	**A** F P **L** C **S** **L** Y **L** I A V L G N	20
26 33	**L** C S **L** Y **L** **I** A **V** L G N L T I	20
27 35	**S** L Y **L** I **A** **V** L **G** N L T I I Y	20
28 39	**I** A V **L** G **N** **L** T **I** I Y I V R T	20
29 42	**L** G N **L** T **I** **I** Y **I** V R T E H S	20
30 44	**N** L T **I** I **Y** **I** V **R** T E H S L H	20
31 48	**I** Y I **V** R **T** **E** H **S** L H E P M Y	20
32 58	**H** E P **M** Y **I** **F** L **C** M L S G I D	20
33 62	**Y** I F **L** C **M** **L** S **G** I D I L I S	20
34 65	**L** C M **L** S **G** **I** D **I** L I S T S S	20
35 71	**I** D I **L** I **S** **T** S **S** M P K M L A	20

HLA-DRB1*0401 (DR4Dw4) 15-mers

(SEQ ID NOS 2672-2805, respectively in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
36	80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	20
37	81	P	K	M	L	A	I	F	W	F	N	S	T	T	I	Q	20
38	91	S	T	T	I	Q	F	D	A	C	L	L	Q	I	F	A	20
39	97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	20
40	98	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	20
41	100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	20
42	103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	20
43	106	I	H	S	L	S	G	M	E	S	T	V	L	L	A	M	20
44	115	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	20
45	117	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	P	20
46	125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	20
47	129	C	H	P	L	R	H	A	T	V	L	T	L	P	R	V	20
48	137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	20
49	140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	20
50	155	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	P	20
51	162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
52	165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	20
53	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	20
54	183	H	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	20
55	186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
56	193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	20
57	196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	20
58	199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
59	200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
60	202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	20
61	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	20
62	206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	20
63	208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	20
64	211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	20
65	212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	20
66	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	20
67	240	G	T	C	V	S	H	V	C	A	V	F	I	F	Y	V	20
68	243	V	S	H	V	C	A	V	F	I	F	Y	V	P	F	I	20
69	246	V	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	20
70	248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	20
71	251	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	F	20
72	272	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	20
73	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	20
74	285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	20
75	18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	18
76	27	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	18
77	69	S	G	I	D	I	L	I	S	T	S	S	M	P	K	M	18
78	94	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	S	18
79	99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	18
80	107	H	S	L	S	G	M	E	S	T	V	L	L	A	M	A	18
81	116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	18
82	126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	18
83	164	F	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	18
84	176	L	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	18

HLA-DRB1*0401 (DR4Dw4) 15-mers

(SEQ ID NOS 2672-2805, respectively in order of appearance)

Pos		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
85	187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
86	205	I	I	S	A	I	G	L	D	S	L	L	I	S	F	S	18
87	233	E	A	Q	A	K	A	F	G	T	C	V	S	H	V	C	18
88	237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	18
89	271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	18
90	293	Y	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	18
91	294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	18
92	10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	16
93	28	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	16
94	59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	16
95	61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	16
96	85	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	16
97	101	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	16
98	177	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	C	16
99	236	A	K	A	F	G	T	C	V	S	H	V	C	A	V	F	16
100	249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	16
101	253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	16
102	13	Y	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	14
103	14	F	I	L	I	G	L	P	G	L	E	E	A	Q	F	W	14
104	16	L	I	G	L	P	G	L	E	E	A	Q	F	W	L	A	14
105	38	L	I	A	V	L	G	N	L	T	I	I	Y	I	V	R	14
106	47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	14
107	54	E	H	S	L	H	E	P	M	Y	I	F	L	C	M	L	14
108	60	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	14
109	64	F	L	C	M	L	S	G	I	D	I	L	I	S	T	S	14
110	70	G	I	D	I	L	I	S	T	S	S	M	P	K	M	L	14
111	72	D	I	L	I	S	T	S	S	M	P	K	M	L	A	I	14
112	109	L	S	G	M	E	S	T	V	L	L	A	M	A	F	D	14
113	113	E	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	14
114	135	A	T	V	L	T	L	P	R	V	T	K	I	G	V	A	14
115	143	V	T	K	I	G	V	A	A	V	V	R	G	A	A	L	14
116	148	V	A	A	V	V	R	G	A	A	L	M	A	P	L	P	14
117	149	A	A	V	V	R	G	A	A	L	M	A	P	L	P	V	14
118	154	G	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	14
119	158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	14
120	173	S	N	I	L	S	H	S	Y	C	L	H	Q	D	V	M	14
121	184	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	V	14
122	191	C	D	D	I	R	V	N	V	V	Y	G	L	I	V	I	14
123	195	R	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	14
124	213	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	V	14
125	220	Y	L	L	I	L	K	T	V	L	G	L	T	R	E	A	14
126	221	L	L	I	L	K	T	V	L	G	L	T	R	E	A	Q	14
127	225	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	F	14
128	259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	14
129	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	14
130	273	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	14
131	274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	14
132	280	I	Y	L	L	V	P	P	V	L	N	P	I	V	Y	G	14
133	284	V	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	14

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
134	302	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	E	14

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	145	K	I	G	V	A	A	V	V	R	G	A	A	L	M	A	28
2	122	F	D	R	Y	V	A	I	C	H	P	L	R	H	A	T	25
3	217	S	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	25
4	197	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	L	24
5	10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	23
6	255	P	F	I	G	L	S	M	V	H	R	F	S	K	R	R	23
7	44	N	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	22
8	59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	22
9	158	M	A	P	L	P	V	F	I	K	Q	L	P	F	C	R	22
10	237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	22
11	74	L	I	S	T	S	S	M	P	K	M	L	A	I	F	W	21
12	134	H	A	T	V	L	T	L	P	R	V	T	K	I	G	V	20
13	137	V	L	T	L	P	R	V	T	K	I	G	V	A	A	V	20
14	162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
15	199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
16	224	L	K	T	V	L	G	L	T	R	E	A	Q	A	K	A	20
17	256	F	I	G	L	S	M	V	H	R	F	S	K	R	R	D	20
18	290	P	I	V	Y	G	V	K	T	K	E	I	R	Q	R	I	20
19	301	R	Q	R	I	L	R	L	F	H	V	A	T	H	A	S	20
20	65	L	C	M	L	S	G	I	D	I	L	I	S	T	S	S	19
21	100	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	19
22	196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	19
23	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	19
24	247	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	19
25	274	P	V	I	L	A	N	I	Y	L	L	V	P	P	V	L	19
26	45	L	T	I	I	Y	I	V	R	T	E	H	S	L	H	E	18
27	68	L	S	G	I	D	I	L	I	S	T	S	S	M	P	K	18
28	80	M	P	K	M	L	A	I	F	W	F	N	S	T	T	I	18
29	97	D	A	C	L	L	Q	I	F	A	I	H	S	L	S	G	18
30	103	I	F	A	I	H	S	L	S	G	M	E	S	T	V	L	18
31	208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	18
32	249	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	H	18
33	61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	17
34	215	L	I	S	F	S	Y	L	L	I	L	K	T	V	L	G	17
35	259	L	S	M	V	H	R	F	S	K	R	R	D	S	P	L	17
36	278	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	V	17
37	288	L	N	P	I	V	Y	G	V	K	T	K	E	I	R	Q	17
38	11	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	A	16
39	24	E	A	Q	F	W	L	A	F	P	L	C	S	L	Y	L	16
40	42	L	G	N	L	T	I	I	Y	I	V	R	T	E	H	S	16
41	253	Y	V	P	F	I	G	L	S	M	V	H	R	F	S	K	16
42	47	I	I	Y	I	V	R	T	E	H	S	L	H	E	P	M	15

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively
in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
43	99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	15
44	116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	15
45	143	V	T	K	I	G	V	A	A	V	V	R	G	A	A	L	15
46	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	15
47	227	V	L	G	L	T	R	E	A	Q	A	K	A	F	G	T	15
48	260	S	M	V	H	R	F	S	K	R	R	D	S	P	L	P	15
49	261	M	V	H	R	F	S	K	R	R	D	S	P	L	P	V	15
50	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	15
51	285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	15
52	114	S	T	V	L	L	A	M	A	F	D	R	Y	V	A	I	14
53	125	Y	V	A	I	C	H	P	L	R	H	A	T	V	L	T	14
54	126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	14
55	140	L	P	R	V	T	K	I	G	V	A	A	V	V	R	G	14
56	170	F	C	R	S	N	I	L	S	H	S	Y	C	L	H	Q	14
57	180	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	I	14
58	193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	14
59	229	G	L	T	R	E	A	Q	A	K	A	F	G	T	C	V	14
60	270	D	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	14
61	298	K	E	I	R	Q	R	I	L	R	L	F	H	V	A	T	14

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Please replace Table XXIX, beginning at page 213, line 1, with the following rewritten Table XXIX:

--Table XXIX. Nucleotide sequence in the 5' region close to 101P3A11 gene (SEQ ID NO: 2867).

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   1 TGCGCTCCAC CAAGCCTGGC TAACTTTTGC ATTTTTAATA GAGGCAGGGT TTCACCATGT
  61 TGGCCTGGCT GGTCTCGAAC CCCTGACCTT GCGATCTGCC CACCTCGGCC TCCCAAAGTG
 121 CTGGGATTAC AGGCGTGAGC CACTGTACCT GGCGGGGCTT ATTGTTTTTT AAAAAGATTT
 181 CCAAAACCTT GCCCTGGCAA TTCTGATTTT CTGGGCCTGG AGCAGGACCT GGAGGGATGG
 241 TGTTGTCAAT TACTTTAGAT GTTTCTATCA GGAAAGTTTG AGAAATGGTA TTCAGGCCTA
 301 AACACAAACC TCTCTTGAAA TCTCATCCCA GACTGAGCCC CTGCTCCCTA TCTTAAATTA
 361 GATTATAGTA GGTCTTAAAG TCAGCTGTAG ACTGAGCCTC TAAATCTGAA CCCAGACCCA
 421 CCCTAACCCC AGGATACATC AGAAGAGCTG GTCAATGTGG ACCATTCTGA GCAATCCTGC
 481 AAGTCTACTC TGATGGGAAA AGGCTAAGAG CAGTGCCCTG GGCAGCAACA TCAGCTCTGA
 541 AGATGCAGGA CTGTGTTACA TGTTTTATGA GTGGGTCTTC ACACACTGAG ATTCATGGGA
 601 CAGTAATAGA ATCTGCTTGT GCAGCACTGG GGCCTTGGAG GGTCAGGGTA AGGCTCAAGA
 661 TGTCCAGGAA GTTGTATATA AGGAGAATCA GAGCAGAGAG AGACTAGGGT TCAGAATTAC
 721 CAGGATGACT TAGTCCTGTT TGTTACTGTC ACCACTCCAA TGCCTTTTCC TCATTAGTCC
 781 TTTCTCTCCT CTGAGCCACA ACTAAATGAT GTTTCTACTT TTCCCTTTCT ACTTTCCTAG
 841 ACCCTGGATT TTGTATGCAG AAGCCCCAGC TCTTGGTCCC TATCATAGCC ACTTCAAATG
 901 GAAATCTGGT CCACGCAGCA TACTTCCTTT TGGTGGGTAT CCCTGGCCTG GGGCCTACCA
 961 TACACTTTTG GCTGGCTTTC CCACTGTGTT TTATGTATGC CTTGGCCACC CTGGGTAACC
1021 TGACCATTGT CCTCATCATT CGTGTGGAGA GGCGACTGCA TGAGCCCATG TACCTCTTCC
1081 TGGCCATGCT TTCCACTATT GACCTAGTCC TCTCCTCTAT CACCATGCCC AAGATGGCCA
1141 GTCTTTTCCT GATGGGCATC CAGGAGATCG AGTTCAACAT TTGCCTGGCC CAGATGTTCC
1201 TTATCCATGC TCTGTCAGCC GTGGAGTCAG CTGTCCTGCT GGCCATGGCT TTTGACCGCT
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1261 TTGTGGCCAT TTGCCACCCA TTGCGCCATG CTTCTGTGCT GACAGGGTGT ACTGTGGCCA
1321 AGATTGGACT ATCTGCCCTG ACCAGGGGGT TTGTATTCTT CTTCCCACTG CCCTTCATCC
1381 TCAAGTGGTT GTCCTACTGC CAAACACATA CTGTCACACA CTCCTTCTGT CTGCACCAAG
1441 ATATTATGAA GCTGTCCTGT ACTGACACCA GGGTCAATGT GGTTTATGGA CTCTTCATCA
1501 TCCTCTCAGT CATGGGTGTG GACTCTCTCT TCATTGGCTT CTCATATATC CTCATCCTGT
1561 GGGCTGTTTT GGAGCTGTCC TCTCGGAGGG CAGCACTCAA GGCTTTCAAC ACCTGCATCT
1621 CCCACCTCTG TGCTGTTCTG GTCTTCTATG TACCCCTCAT TGGGCTCTCG GTGGTGCATA
1681 GGCTGGGTGG TCCCACCTCC CTCCTCCATG TGGTTATGGC TAATACCTAC TTGCTGCTAC
1741 CACCTGTAGT CAACCCCCTT GTCTATGGAG CCAAGACCAA AGAGATCTGT TCAAGGGTCC
1801 TCTGTATGTT CTCACAAGGT GGCAAGTGAG ACACCTTAGT GTCTCGCTTC TACTACTACT
1861 ACAGAAGATG GGAATATTAG GATCCTATTG AATGCCTTGG TGATTAAAGT ATCAAACCTA
1921 TTGTGCTGTC TTCTTCCAGC AATTTAAGTA GATCATGTAT TCTGTCTCCA GGAATGTGTC
1981 AGTACTGAAC TTATGACCCT GTCTGGACAT CCTGGAGAAT GACTGCACTA GTCCCTCTGC
2041 TATGGTGGTC TTGCCTTCTC CTTCTCTCTC AGCTAGAAAA TACATCTAGT TTTGACATGG
2101 GGAGGCTGTA AAGATCACAC CTCATGGTTC ATTCCAGTTT TGAAGTATGA TTTTAATGTT
2161 CTTGCCCCCA TGTGCCCATG TTGGTGAATT TGCATGGACT ATAAACGTTA TTGCAAATAC
2221 CCTAAAGTGG TTACCCAGCC ATAATCAGGG GTTAATGAAG GTATTTGGGG AATAGTAACT
2281 GGAGAGACAG CAACAAGACA AGAGGCAGCT CACATGCAAT GTTGAAGTTT CTGTATGCAA
2341 GAGGGTGTGT TGGCAGATTT GTGAAATCTG CCCATTTGCA TCTGTATGGC TCTATATGAC
2401 TATTTGTCCA TAAGGGTGCC ATGTATTCTG GTTGTGGGTG TGAATGTGTG GGTGTGTTTA
2461 TGTGGACACT TGCTTTTCAG TGTGCGTATA TGTGAGAGAG AGGGTGCACA CATGGAATAC
2521 GTACTGGTTG TGTCCTGGTG AGTGTGGTAG CTATGTCCTG GCACATGTAT GTTTCATGAG
2581 ACGTGTCTCT GATTGCGCAT TTGTATTTCT GTGGTATCTG TTAGTTGGTA TATGATATGT
2641 GTCTACGTGA GAATGCTGGT GTCTGTATCT GCATGGTGGG CAGTACCTTT ATGTGTATCT
2701 GGTAAGAATG CTGCCTCTAC CTTTTCTTCC TATTTGTACT ATGTGAATGT GGTGCATGAA
2761 TGTGTGGAAT GTGTGGAATG TGTAGTATTG GGATGCCTGT ATCTTTCAGC GTGTTTGGGT
2821 GTATGTCCAC TGTGCATAAT ATTTGAGATG TAAAACCATT TTGTGCGGTA TATGTGTTAT
2881 TAGTTGTAAG TCGGTGAAAT GTACATCTGA ATTCTGTGTG CATATTGTTG GTACTGATGC
2941 TATTTTCGTG CATATGTCTA GTGTATATGT TTTAAGGCAA ACTTTCTTTG TGTGTTGGGT
3001 GTGTATGTGA CACGAATGGG GACAGCATCT GTATTTCTGA GCATGGATTG ATGTGTGGTG
3061 TCTGTATGTA TCTTGGAATG GAGGAGGGAG ATTGAAGAAG TCTGGCTGTG AGCAGCAGAA
3121 ATAATTTCCA AAGTTGAGTG ACATGACTCT AAGATGCCCA GTTTCTCGGC CTGGGGTCAG
3181 CCTGGGTGAT AGCTCAGTCT GTCAGAATGA AAGGAAACAC GGTGCTTCCT TGCTCCACCT
3241 TTTCACAGGC CAGACCACAC CTTCTTCATC CTGAACACAA GGATTTCAAG GGCTTTTGTT
3301 ACCTCTTCCT ACGTTTCCTG CCTCTGCTAT CCGAGGCACT GGCCTCCCTA AACCCTGCCC
3361 TCCTGCCTCA ATAGCAAGTC ATGGTATCCT CACCTCTCCC TTCCCTTTTT GGCTTATCTG
3421 CCAAACATGT ATAAAAGTCC TTGGTTCCCC ATCTCTACTA AAAATACAAC AATTAGCCGG
3481 GTGTGATGGC GCGTGCCTGT AGTCCCAGCT AGTTGGGAGG CTGAGGCAGG AGAAACGCTT
3541 GAGCCCGCAA GGTGGAGGTT GCAGTGAGCC GAGATCATGC CACTGCACTC CAGCCTGGTG
3601 ACAGAGCAAG ACTCTGTGTC AAAAAAAAAA AAAAAAAAAA AGCCTTGGTT GTAGGGAGTT
3661 TCTCCTAATC CCTCTGGGAA AGCAAGGGTG GAGGGGAAGC CAGTCAATCT CCCTTCTGTT
3721 GCCGCATGGA AACTCCCTTA AGGCAGGAAG CTGAAAAAAC TGTAGCATTC ACCTCATTAT
3781 TCACCTTGTC TCATGTCTCA CTGTCCTTCC ACATGTCTCA TTGTTACTCC ATATTGGATG
3841 GAAGTAGAAG TCCCTTTGGT ATTTTTTAAA GTCTTTGCCA TGTCTAAGTT AATGAGGTTA
3901 ATGGAGGCAG CAGAGATGGC TCCAGGGTTC TGATAGCAAG TGTCAGGCTG CGTGCTCTGT
3961 AGGCACCAGA AACTGTTGTC ACCAGTAATT TTGATGTGGT CTGAGTTAGA ATGGTCTGAT
4021 TTGCCATGAT CTATTTAACA TAGCTTGATT TAGCGTGTCC TGTGTTCTGA ATTTAAAACT
4081 CACAGTTGTG AAACTGATCA GTAAAAAATA AGGGGAGACC AACTAAAAAC CATGTTGTTC
4141 TATTTATAGA TGTAGTTTTT ACTTATTTCA AAATACGAGG TATTTAGTTT TACATTCAAA
4201 TTGTTCTCTA ACTCTCTAAA ATGTTCTCTG ACTATTTTTG CCCTTAAGGG AGAAACCAGA
4261 TGTCATTGGT CTTACGTGGC TGGTGTTGGG GGTGGGGAGG GTTAAAGAAA CCACGTTCTC
4321 TGTCCTCAGC CAGAAGTTCA GTAATCCAAG GCCAGAGAGT GGACGGCAGA GGCACTGTCC
4381 CTGGGGACCT TGGTTATAAG TTATCCAGAC ACAGGGACCA GAGCCTGGGA GACAAAAAAA
4441 GATGTAGCCC TAGGGCTTTG GGAAAAGGAG GATGGACCCA GTGAATTCCA CGCTTAGCAA
```

```
4501 GGACCTAAAC AGTGTCCCCC AAATGAGAGA AGGGAGGACA GAAAGAACAC TTCAGGATGG
4561 AAATGGGCTG ACACTTAACC GTGGAGTGTC TCTGCAAACT TCCTTTGCCA TTCTCCTGTT
4621 TGAGTTTGAT AAACCTGAGA AGAGACTTGG ATAAAGACCG TCACGAAGAC TACACTAATG
4681 AGTTTCTTCT AGCTTTTTTC TACTCACTTT CCCTATCTAT CCTTCACATT GGGAGTTGGC
4741 ATGAGGATCC CAGCAGCCCA TCAGGGGAGG ACTCTAGAGA TCCCTTTCCC CATTGCCTCT
4801 CCTCCCCATA CCCCCAGGCA TATCCTCCCA GGGCACGGAA GCTGAGAAGC AGTCCAGAAC
4861 CACAGTGGGC TAGTGAGGGG TACCTGCTGA TGTACCCTTT GGACAGCATT CTGCCCCACC
4921 CTGCAGGAAG AAGCAGAAGG AGGGAGAGGG TGAGGCAGAG AATAAATAAC CCTGACCAGG
4981 GAGGTCCAAG GGAGTAGGCG GAGAcagaga ggctgtattt cagtgcagcc tgccagacct
```

Note: The three high score predictions of promoters were bold and underlined. The lower case sequence indicates the beginning part of the transcript of 101P3A11 gene.--

Please replace Table XXX, beginning at page 214, line 35, with the following rewritten Table XXX:

--Table XXX: Promoters and their positions predicted by Neural Network Promoter Prediction computer program. (various portions of SEQ ID NO: 2867, respectively, in order of appearance)

Start	End	Score	Promoter Sequence
25	75	0.91	TTTTGCATTTTTAATAGAGGCAGGGTTTCACCATGTTGGCCTGGCTGGTC
665	715	0.95	CAGGAAGTTGTATATAAGGAGAATCAGAGCAGAGAGAGACTAGGGTTCAG
2477	2527	0.91	TCAGTGTGCGTATATGTGAGAGAGAGGGTGCACACATGGAATACGTACTG
3139	3189	0.82	TGACATGACTCTAAGATGCCCAGTTTCTCGGCCTGGGGTCAGCCTGGGTG
3420	3470	0.96	GCCAAACATGTATAAAAGTCCTTGGTTCCCCATCTCTACTAAAAATACAA
4092	4142	0.99	AACTGATCAGTAAAAAATAAGGGGAGACCAACTAAAAACCATGTTGTTCT
4953	5003	0.97	AGGCAGAGAATAAATAACCCTGACCAGGGAGGTCCAAGGGAGTAGGCGGA--

Please replace Table XXXI, beginning at page 215, line 1, with the following rewritten Table XXXI:

--Table XXXI: Alignment of five homologous 5' upstream genomic regulatory regions of the human 101P3A11 and PSA genes.

Query: 5' upstream regulatory region of the PSA gene
Subject: Putative 5' upstream regulatory region of the 101P3A11 gene.
Nucleic acid sequences predicted to be binding sites for the indicated transcription factors are **bolded**, underlined, or *italicized*.

```
1.                    NF-1 SP-1 NF-1
Query: 3864 ccaggctggagtgcagtggcgcagtctcggctcactgcaacctctgcctcccaggttcaa 3923
(SEQ ID NO: 2868)
            ||||||||||||||||||||    ||||||||||||||||||||  |||  | ||  ||||
Sbjct: 3598 ccaggctggagtgcagtggcatgatctcggctcactgcaacctccaccttgcgggctcaa 3539
(SEQ ID NO: 2869)

Query: 3924 gtgattctcctgcctcagcctcctgagttgctgggattacaggcatgcagcaccatgccc 3983
            | | ||||||||||||||||||||  | | |||||||  ||||||||  ||  ||  ||  |||
Sbjct: 3538 gcgtttctcctgcctcagcctcccaactagctgggactacaggcacgcgccatcacaccc 3479

Query: 3984 agctaatttttgtatttttagtagagatgggg 4015
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                |||||||  |||||||||||||||||||||||||
Sbjct: 3478 ggctaattgttgtatttttagtagagatgggg 3447
```

2.

```
Query: 4670 cctgtaatcccagctactgaggaggctgaggcaggagaatcacttgaacccagaaggcag 4729
(SEQ ID NO: 2870)
             ||||||  |||||||||  |  ||||||||||||||||||  | |||||  |||  ||||  |
Sbjct: 3496 cctgtagtcccagctagttgggaggctgaggcaggagaaacgcttgagcccgcaaggtgg 3555
(SEQ ID NO: 2871)
                                                SP1                    NF-E
                                      NF-1      NF-1          GR        GR
Query: 4730 aggttgcaatgagccgagattgcgccactgcactccagcctgggtgacagagtgagactc 4789
             ||||||||  ||||||||||   ||||||||||||||||||  |||||||||  ||||||
Sbjct: 3556 aggttgcagtgagccgagatcatgccactgcactccagcct-ggtgacagagcaagactc 3614

Query: 4790 tgtctcaaaaaaaaaaaa 4807
             |||  ||||||||||||||
Sbjct: 3615 tgtgtcaaaaaaaaaaaa 3632
```

3.

```
                          GR            NF-1 SP1
Query: 142  tgagactgagtctcgctctgtgcccaggctggagtgcagtggtgcaaccttggctcactg 201
(SEQ ID NO: 2872)
             |||  ||  ||||||  |||||||  ||||||||||||||||||     | ||  |||||||||
Sbjct: 3621 tgacacagagtcttgctctgtcaccaggctggagtgcagtggcatgatctcggctcactg 3562
(SEQ ID NO: 2873)

Query: 202  caagctccgcctcctgggttcacgccattctcctgcctcagcctcctgagtagctgggac 261
             |||  ||||  |||   |||  |||  ||  |||||||||||||||||||  | ||||||||||
Sbjct: 3561 caacctccaccttgcgggctcaagcgtttctcctgcctcagcctcccaactagctgggac 3502

                     NF-1
Query: 262  tacaggcacccgccaccacgcctggctaannnnnnngtatttttagtagagatgggg 318
             |||||||||  |||||  |||  ||  ||||||       ||||||||||||||||||||
Sbjct: 3501 tacaggcacgcgccatcacacccggctaa--ttgttgtatttttagtagagatgggg 3447
```

4.

```
Query: 300 atttttagtagagatggggtttcactgtgttagccaggatggtctcagtctcctgacctc 359
(SEQ ID NO: 2874)
            |||||||  |||||   |||||||||  ||||  |||  ||  |||||||   | ||||||||
Sbjct: 31  atttttaatagaggcagggtttcaccatgttggcctggctggtctcgaacccctgacctt 90
(SEQ ID NO: 2875)
                  SP1                                                    NF-1
                LF-A1                                                    CP2
Query: 360 gtgatctgcccaccttggcctcccaaagtgctgggattacaggcgtgagccactgcgcct 419
             | ||||||||||||| ||||||||||||||||||||||||||||||||||||||||  |||
Sbjct: 91  gcgatctgcccacctcggcctcccaaagtgctgggattacaggcgtgagccactgtacct 150

          NF-1
Query: 420 ggc 422
             |||
Sbjct: 151 ggc 153
```

5.

```
                          NF-1
            NF-1       CP2
Query: 4506 gccaggcacagtggctcacgcctgtaatcccaacaccatgggaggctgagatgggtggat 4565
(SEQ ID NO: 2876)
            |||||| |||||||||||||||||||||||| |||  |||||||| ||| ||||  |||
Sbjct: 153  gccaggtacagtggctcacgcctgtaatcccagcactttgggaggccgaggtgggcagat 94
(SEQ ID NO: 2877)

Query: 4566 cacgaggtcaggagtttgagaccagcctgaccaacatggtgaaactctgtctcta 4620
            | | |||||||| ||| |||||||||| | ||||||||||||||| ||| |||||
Sbjct: 93   cgcaaggtcaggggttcgagaccagccaggccaacatggtgaaaccctgcctcta 39--
```

REMARKS

The Specification has been amended to correct erroneous sequence identification numbers and include sequence identification numbers which were omitted at the time of filing.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "**Version with markings to show changes made.**".

The undersigned hereby states that the compact disc copy of the Sequence Listing and the computer readable form copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.825(a) and (b), respectively, are the same and contain no new matter. Accordingly, entry of the Sequence Listing into the above-captioned case is respectfully requested.

In the unlikely event that the patent office determines that extensions and/or other relief is required, applicant petition for any required relief including extensions of time and authorize the assistant commissioner to charge the cost of such petitions and/or fees due to our deposit account no. 03-1952 under order no. 511582002420. The assistant commissioner is not authorized to charge the cost of the issue fee to the deposit account.

Respectfully submitted,

Dated: May 20, 2002

By: Kate H. Murashige

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

The paragraph beginning at page 7, line 21, has been amended as follows:

Figure 1. 101P3A11 SSH sequence (SEQ ID NO:2960). The 101P3A11 SSH sequence.

The paragraph beginning at page 7, line 22, has been amended as follows:

Figures 2A-2D. The cDNA (SEQ ID. NO. :2961) and amino acid sequence (SEQ ID. NO. :2962) of 101P3A11. The start methionine is underlined. The open reading frame extends from nucleic acid 133 to 1086 including the stop codon (the codon for the initial M is omitted as the shorter peptide has a more favorable Kozak sequence).

The paragraph beginning at page 7, line 26, has been amended as follows:

Figure 3. Amino acid sequence of 101P3A11 (SEQ ID. NO. :piece of 2962). The 101P3A11 protein has 317 amino acids.

The paragraph beginning at page 7, line 28, has been amended as followsh:

Figure 4. Alignment of 101P3A11 (Sbjct) (SEQ ID NO: 2964) with mouse olfactory receptor S25 (Query.) (SEQ ID NO: 2963) The transmembrane regions of 101P3A11 and mouse olfactory receptor S25 (ORS25)predicted using the TMHMM algorithm are highlighted in gray. The amino acids of ORS25 predicted (Floriano, W.B., et al, 2000, Proc. Natl. Acad. Sci., USA, 97:10712-10716) to be involved in binding of the ligand hexanol and/or involved in the formation of the ligand binding pocket are italicized and bolded in the Figure, and are: Leu 131, Val 134, Val 135, Gly 138, Thr139, Ser 193, Ser 197, Phe 225, Ala 230, Ile 231, Gly 234, Thr 284, Phe 287, Gln 300, Lys 302.

The paragraph beginning at page 11, line 31, has been amended as follows:

Figure 23. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2965) with the rat (SEQ ID NO: 2966) GPCR RA1C (gi|3420759). Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%).

The paragraph beginning at page 12, line 1, has been amended as follows:

Figure 24. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2967) with the human prostate specific GPCR (SEQ ID NO: 2968) (gi|13540539). Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%).

The paragraph beginning at page 12, line 3, has been amended as follows:

Figure 25. Alignment of 101P3A11-PHOR-1 (Phor) (SEQ ID NO: 2969) with human olfactory receptor 5II12, HOR5 (SEQ ID NO: 2970) (gi|14423836). Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%).

The paragraph beginning at page 36, line 20, has been amended as follows:

Also, different MHC class I molecules prefer a different length of ligands. For example, SYFPEITHI offers predictions for H2-Kb octamers, HLA-A*0201 nonamers and decamers, or HLA-B8 octamers and nonamers. The maximal scores vary between different MHC alleles. Therefore, one can include known ligands/epitopes in order to have an approximation of the scoring. For example, the maximal score for HLA-A*0201 peptides is 36. The well-known epitope GILGFVFTL (SEQ ID NO: 1401) derived from the influenza A matrix protein scores 30. All predicted MHC class II ligands are 15mers, consisting of three N-terminal flanking residues, the nonamer core sequence located within the binding groove, and three C-terminal flanking residues. Thus, anchor residue P1 appears in position 4 of the peptides predicted with "SYFPEITHI".

The paragraph beginning at page 37, line 25, has been amended as follows:

In an embodiment described in the examples that follow, 101P3A11 can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 101P3A11 with a C-terminal 6XHis (SEQ ID NO: 1402) and MYC tag (pcDNA3.1/mycHIS, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 101P3A11 protein in transfected cells. The secreted HIS-tagged 101P3A11 in the culture media can be purified, e.g., using a nickel column using standard techniques.

The paragraph beginning at page 70, line 3, has been amended as follows:

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE; [SEQ ID NO: 710] (SEQ ID NO: 1403), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; [SEQ ID NO: 711] (SEQ ID NO: 1404), and *Streptococcus* 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; [SEQ ID NO: 712] (SEQ ID NO: 1405). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

The paragraph beginning at page 70, line 11, has been amended as follows:

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVAAWTLKAAa [SEQ ID NO: 713] (SEQ ID NO: 1406), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

The paragraph beginning at page 80, line 16, has been amended as follows:

Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant

polynucleotide vectors encoding such single chain antibodies in order to precisely target the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL (SEQ ID NO: 1407) amino acid motif. Intrabodies intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.

The paragraph beginning at page 86, line 29, has been amended as follows:

pGEX Constructs: To generate recombinant 101P3A11 proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 101P3A11 cDNA protein coding sequence are fused to the GST gene by cloning into pGEX-6P-1 or any other GST- fusion vector of the pGEX family (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) (SEQ ID NO: 1402) at the carboxyl-terminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag (SEQ ID NO: 1402) is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScission™ recognition site in pGEX-6P-1, can be employed that permits cleavage of the GST tag from 101P3A11-related protein. The ampicillin resistance gene and pBR322 origin permit selection and maintenance of the pGEX plasmids in *E. coli*. In one embodiment, amino acids 86-317 are cloned into the pGEX-2T expression vector, the protein is expressed and purified.

The paragraph beginning at page 87, line 8, has been amended as follows:

pMAL Constructs: To generate, in bacteria, recombinant 101P3A11 proteins that are fused to maltose-binding protein (MBP), all or parts of the 101P3A11 cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors

(New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 101P3A11 protein sequences with MBP fused at the amino-terminus and a 6X His (SEQ ID NO: 1402) epitope tag at the carboxyl-terminus. The MBP and 6X His tags (SEQ ID NO: 1402) permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His (SEQ ID NO: 1402) epitope tag is generated by adding 6 histidine (SEQ ID NO: 1402) codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 101P3A11. The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds. In one embodiment, amino acids 86-310 is cloned into the pMAL-c2X expression vector, the protein is expressed and purified.

The paragraph beginning at page 87, line 20, has been amended as follows:

pET Constructs: To express 101P3A11 in bacterial cells, all or parts of the 101P3A11 cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 101P3A11 protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His (SEQ ID NO: 1402) and S-Tag ™ that aid purification and detection of the recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 101P3A11 protein are expressed as amino-terminal fusions to NusA.

The paragraph beginning at page 88, line 19, has been amended as follows:

pcDNA4/HisMax Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF was cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has Xpress™ and six histidine (6X His) (SEQ ID NO: 1402) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and

simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

The paragraph beginning at page 88, line 28, has been amended as follows:

pcDNA3.1/MycHis Constructs: To express 101P3A11 in mammalian cells, the 101P3A11 ORF, with a consensus Kozak translation initiation site, was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the myc epitope and 6X His (SEQ ID NO: 1402) epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene can be used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

The paragraph beginning at page 89, line 16, has been amended as follows:

PAPtag: The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of the 101P3A11 proteins while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of 101P3A11 proteins. The resulting recombinant 101P3A11 proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His (SEQ ID NO: 1402) epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

The paragraph beginning at page 89, line 27, has been amended as follows:

ptag5: The 101P3A11 ORF, or portions thereof, of 101P3A11 are cloned into pTag-5. This vector is similar to pAPtag but without the alkaline phosphatase fusion. This construct generated 101P3A11 protein with an amino-terminal IgGκ signal sequence and myc and 6X His (SEQ ID NO: 1402) epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 101P3A11 protein was optimized for secretion into the media of transfected mammalian cells, and was used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 101P3A11 proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

The paragraph beginning at page 90, line 30, has been amended as follows:

Additional pSRα constructs are made that fuse an epitope tag such as the FLAG™ tag to the carboxyl-terminus of 101P3A11 sequences to allow detection using anti-Flag antibodies. For example, the FLAG™ sequence 5' gat tac aag gat gac gac gat aag 3' (SEQ ID NO: 1408) is added to cloning primer at the 3' end of the ORF. Additional pSRα constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His (SEQ ID NO: 1402) fusion proteins of the full-length 101P3A11 proteins.

The paragraph beginning at page 141, line 31, has been amended as follows:

The generation of anti-101P3A11 polyclonal Ab (pAb) using an amino-terminal peptide encoding amino acids 1-14 (MVDPNGNESSATYF; [SEQ ID NO:YY] (SEQ ID NO: 1409) as antigen was reported in our Priority Application. The effect of this antibody on 101P3A11 mediated ERK phosphorylation (Figure 38) and cAMP accumulation (Figure 39) was determined. 293T cells were transfected with control or 101P3A11 cDNA. Cells were allowed to rest overnight, and treated with anti-101P3A11 or control Ab in the presence of 0.5% or 10% FBS. Cells were lysed and analyzed by Western blotting with anti-Phospho-ERK and anti-ERK mAb. Figure 38 shows that expression of 101P3A11 induces ERK phosphorylation in cells treated with 0.5 or 10% FBS. Anti-101P3A11 pAb reduced the phosphorylation of ERK in

293T-101P3A11 cells treated with 0.5% FBS. The ERK overlay demonstrated equal loading, supporting the specificity of this data.

Table XIX, beginning at page 186, has been amended as follows:

Table XIX: Motifs and Post-translational Modifications of 101P3A11

N-glycosylation site
Number of matches: 3
1 7-10 NESS (SEQ ID NO: 1410)
2 44-47 NLTI (SEQ ID NO: 1411)
3 90-93 NSTT (SEQ ID NO: 1412)

cAMP- and cGMP-dependent protein kinase phosphorylation site
268-271 RRDS (SEQ ID NO: 1413)

Protein kinase C phosphorylation site
266-268 SKR

Casein kinase II phosphorylation site
Number of matches: 3
1 56-59 SLHE (SEQ ID NO: 1414)
2 69-72 SGID (SEQ ID NO: 1415)
3 110-113 SGME (SEQ ID NO: 1416)

N-myristoylation site
Number of matches: 4
1 6-11 GNESSA (SEQ ID NO: 1417)
2 21-26 GLEEAQ (SEQ ID NO: 1418)
3 111-116 GMESTV (SEQ ID NO: 1419)
4 240-245 GTCVSH (SEQ ID NO: 1420)

G-protein coupled receptors family 1 signature
112-128 MESTVLLAMAFDRYVAI (SEQ ID NO: 1421)

Table XXI, beginning at page 190, line 1, has been amended as follows:

Table XXI: Nucleotide sequence of the splice variant (SEQ ID NO: 1422)

```
   1 CACATTCCTT CCATACGGTT GAGCCTCTAC CTGCCTGGTG CTGGTCACAG TTCAGCTTCT
  61 TCATGATGGT GGATCCCAAT GGCAATGAAT CCAGTGCTAC ATACTTCATC CTAATAGGCC
 121 TCCCTGGTTT AGAAGAGGCT CAGTTCTGGT TGGCCTCCCA TTGTGCTCCC TCTANCTATG
 181 CTGTGCTAGT AATTGACAAT CATCTACATG TGCGGACGAG CACGNCGCNG AGCCCNGTAT
 241 NATTCTGCNG CTTCAGCATG ACACCCTNCA GTCTCAGCCA AAGNGCATCT CNGTCAATCA
 301 NACACNTGAG CTGTCGTACG AGTTGCATCA TCCTANGGCA GGATCAATGT GCGGNAGGCN
```

```
361 TGACGCAGTG CACGTACCAT GGCAGCAAGA CAGGGCCGGT ACAAATGGGG GCGAGNCGGG
421 GTGAAGATGN ACCCTCGGGT CANAGAGTGC CTCTGCGCCA AAACCTCCAT CATGNNAACA
481 GNGTATAACG GCGNAGAATC GGNNANGCGC AAGGCTAAGG AAANNCCCAA NNCNGGTACT
541 TTAACCCNGC AAANGGCANC NAAACGGGNG GGTNANTGAA CAAGGAAGGN NTGNAACTGG
601 GCCAAAACGG GNTGGGCAAN NNAAGGACTC ATGGGNCCAA GGGACGGNAA AAGGGGNAAN
661 CGGGGCGAAA TGNNAAAAAC CGGGNCCCGG GGAANAANGA AGGGGAANAN GNGTGAAGGA
721 CNGGGTTCAA GGGAAAAGNA AAACCANGGG NNAGAAACCN TTCNAANGGC CCGGGNANGA
781 AAGGAANTNN GNNNGGNGAA AAAATCNAAA AAAAGCNGNG GCNNAAAAAN GGGGGGAANN
841 NAAANACCNN GGNCGNNAAA AAACNNAANG NGGGGGGANT ANACACGGAA ANNNANGGGC
901 GNNNAAGGGA AATAANNCGG GAACNAAAGN GCAAACCGNA CGGNAGGAAC GAAACCCACC
961 GGAGNCGCNN AACGCCNNNC NNANCCCGAG CNGAGGTNG
```

Table XXII, beginning at page 190, line 38, has been amended as follows:

Table XXII: Nucleotide sequence alignment of 101P3A11 with the splice variant.

Score = 337 bits (175), Expect = 4e-89
Identities = 215/223 (96%), Gaps = 6/223 (2%)
Strand = Plus / Plus

```
101P3A11: 68  cacattccttccatacggttgagcctctacctgcctggtgctggtcacagttcagcttct 127
(SEQ ID NO: 1423)
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Variant : 1   cacattccttccatacggttgagcctctacctgcctggtgctggtcacagttcagcttct 60
(SEQ ID NO: 1424)

101P3A11: 128 tcatgatggtggatcccaatggcaatgaatccagtgctacatacttcatcctaataggcc 187
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Variant : 61  tcatgatggtggatcccaatggcaatgaatccagtgctacatacttcatcctaataggcc 120

101P3A11: 188 tccctggtttagaagaggctcagttctggttggccttcccattgtgctccctctacctta 247
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||| ||
Variant : 121 tccctggtttagaagaggctcagttctggttggcc-tcccattgtgctccctctanct-- 177

101P3A11: 248 ttgctgtgctaggtaacttgacaatcatctacattgtgcggac 290
              |||||||||| |||| |||||||||||||||| |||||||||
Variant : 178 atgctgtgcta-gtaa-ttgacaatcatctaca-tgtgcggac 217
```

Table XXIII, beginning at page 191, line 8, has been amended as follows:

Table XXIII: Longest single amino acid sequence alignment of 101P3A11 and the splice variant.

Score = 134 bits (287), Expect(2) = 3e-29
Identities = 51/51 (100%)
Frame = +1 / +3

```
101P3A11: 70  HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 222
(SEQ ID NO: 1425)
              HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA
Variant : 3   HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLA 155
(SEQ ID NO: 1426)
```

Table XXIV, beginning at page 191, line 16, has been amended as follows:

Table XXIV: Peptide sequences from the translation of the nucleotide sequence of the splice variant .

Open reading frame	Amino acid sequences
Frame 1 (SEQ ID NO: 1427)	HIPSIRLSLYLPGAGHSSASS*WWIPMAMNPVLHTSS**ASLV*KRLSSGWPPIVLPLXM LC**LTIIYMCGRARRXAXYXSAASA*HPXVSAKXHLXQSXT*AVVRVASSXGRINVRXA *RSARTMAARQGRYKWGRXGVKMXPRVXECLCAKTSIMXTXYNGXESXXRKAKEXPXXGT LTXQXAXKRXGX*TRKXXNWAKTGWAXXGLMGPRDGKRGXRGEMXKTGXRGXXKGXXXEG XGSREKXNXGXETXXXARXXKEXXXXKKSKKSXGXKXGGXXXPXXXKNXXXGXXTRKXXG XXGK*XGNXXANRTXGTKPTGXAXRXXXPEXRX
Frame 2(SEQ ID NO: 1428)	TFLPYG*ASTCLVLVTVQLLHDGGSQWQ*IQCYILHPNRPPWFRRGSVLVGLPLCSLXLC CASN*QSSTCADEHXAEPXXILXLQHDTLQSQPKXISVNXTXELSYELHHPXAGSMCGRX DAVHVPWQQDRAGTNGGEXG*RXTLGSXSASAPKPPSXXQXITAXNRXXARLRKXPXXVL *PXKXXXNGXVXEQGRXXTGPKRXGQXKDSWXQGTXKGXXGAKXXKPGPGEXXRGXXVKD XVQGKXKTXGXKPFXXPGXERXXXXXKNXKKAXAXKXGEXKXXGRXKTXXGGXXHGXXXA XKGNXXGTKXQTXRXERNPPEXXNAXXXPSXG
Frame 3(SEQ ID NO: 1429)	HSFHTVEPLPAWCWSQFSFFMMVDPNGNESSATYFILIGLPGLEEAQFWLASHCAPSXYA VLVIDNHLHVRTSTXXSPVXFCXFSMTPXSLSQXASXSIXHXSCRTSCIILXQDQCAXGX TQCTYHGSKTGPVQMGAXRGEDXPSGXRVPLRQNLHHXNXV*RRRIGXAQG*GXXQXXYF NPAXGXXTGGXXNKEGXXLGQNGXGXXRTHGXKGRXKGXXGRNXKNRXPGXXEGEXX*RT GFKGKXKPXXRNXSXGPGXKGXXXGEKIXKKXXXKXGGXXXTXXXKKXXXGGXXTEXXGR XREIXREXKXKPXGRNETHRXRXTPXXXRAEV

Note: Frame 3 gives the longest subsequence that is identical with 101P3A11 amino acid sequence. In this Table each (*)indicates the product of a single stop codon, and 'X' indicates a single unknown amino acid.

Table XXVI, beginning at page 193, line 1, has been amended as follows:

Table XXVI:

HLA Class I Nonamers (SEQ ID NOS 1430-1462, respectively in order of appearance)

HLA-A1 nonomers

	Pos	1	2	3	4	5	6	7	8	9	score
1	245	H	V	**C**	A	V	F	I	F	**Y**	24
2	29	L	A	**F**	P	L	C	S	L	**Y**	21
3	41	V	L	**G**	N	L	T	I	I	**Y**	21
4	285	P	P	**V**	L	N	P	I	V	**Y**	20
5	111	G	M	**E**	S	T	V	L	L	**A**	19
6	117	L	L	**A**	M	A	F	D	R	**Y**	19
7	172	R	S	**N**	I	L	S	H	S	**Y**	19
8	192	D	D	**I**	R	V	N	V	V	**Y**	19
9	212	D	S	**L**	L	I	S	F	S	**Y**	19
10	57	L	H	**E**	P	M	Y	I	F	**L**	18
11	22	L	E	**E**	A	Q	F	W	L	**A**	17
12	9	S	S	**A**	T	Y	F	I	L	**I**	16
13	52	R	T	**E**	H	S	L	H	E	**P**	16
14	54	E	H	**S**	L	H	E	P	M	**Y**	16

HLA-A1 nonomers

	Pos	1	2	3	4	5	6	7	8	9	score
15	78	S	S	**M**	P	K	M	L	A	**I**	16
16	95	Q	F	**D**	A	C	L	L	Q	**I**	16
17	159	A	P	**L**	P	V	F	I	K	**Q**	16
18	183	H	Q	**D**	V	M	K	L	A	**C**	16
19	1	M	V	**D**	P	N	G	N	E	**S**	15
20	5	N	G	**N**	E	S	S	A	T	**Y**	15
21	210	G	L	**D**	S	L	L	I	S	**F**	15
22	273	L	P	**V**	I	L	A	N	I	**Y**	15
23	271	S	P	**L**	P	V	I	L	A	**N**	14
24	91	S	T	**T**	I	Q	F	D	A	**C**	13
25	121	A	F	**D**	R	Y	V	A	I	**C**	13
26	138	L	T	**L**	P	R	V	T	K	**I**	13
27	218	F	S	**Y**	L	L	I	L	K	**T**	13
28	282	L	L	**V**	P	P	V	L	N	**P**	13
29	190	A	C	**D**	D	I	R	V	N	**V**	12
30	191	C	D	**D**	I	R	V	N	V	**V**	12
31	231	T	R	**E**	A	Q	A	K	A	**F**	12
32	268	R	R	**D**	S	P	L	P	V	**I**	12
33	270	D	S	**P**	L	P	V	I	L	**A**	12

HLA-A*0201 nonomers (SEQ ID NOS 1463-1569, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	287	V	**L**	N	P	I	V	Y	G	**V**	30
2	14	F	**I**	L	I	G	L	P	G	**L**	29
3	28	W	**L**	A	F	P	L	C	S	**L**	28
4	37	Y	**L**	I	A	V	L	G	N	**L**	28
5	222	L	**I**	L	K	T	V	L	G	**L**	28
6	66	C	**M**	L	S	G	I	D	I	**L**	26
7	108	S	**L**	S	G	M	E	S	T	**V**	26
8	181	C	**L**	H	Q	D	V	M	K	**L**	26
9	201	G	**L**	I	V	I	I	S	A	**I**	26
10	214	L	**L**	I	S	F	S	Y	L	**L**	26
11	275	V	**I**	L	A	N	I	Y	L	**L**	26
12	157	L	**M**	A	P	L	P	V	F	**I**	25
13	220	Y	**L**	L	I	L	K	T	V	**L**	25
14	276	I	**L**	A	N	I	Y	L	L	**V**	25
15	279	N	**I**	Y	L	L	V	P	P	**V**	25
16	138	L	**T**	L	P	R	V	T	K	**I**	24
17	213	S	**L**	L	I	S	F	S	Y	**L**	24
18	49	Y	**I**	V	R	T	E	H	S	**L**	23
19	143	V	**T**	K	I	G	V	A	A	**V**	23
20	188	K	**L**	A	C	D	D	I	R	**V**	23
21	198	V	**V**	Y	G	L	I	V	I	**I**	23
22	21	G	**L**	E	E	A	Q	F	W	**L**	22
23	40	A	**V**	L	G	N	L	T	I	**I**	22
24	206	I	**S**	A	I	G	L	D	S	**L**	22
25	11	A	**T**	Y	F	I	L	I	G	**L**	21
26	60	P	**M**	Y	I	F	L	C	M	**L**	21
27	135	A	**T**	V	L	T	L	P	R	**V**	21

HLA-A*0201 nonomers (SEQ ID NOS 1463-1569, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
28	160	P	**L**	P	V	F	I	K	Q	**L**	21
29	174	N	**I**	L	S	H	S	Y	C	**L**	21
30	207	S	**A**	I	G	L	D	S	L	**L**	21
31	272	P	**L**	P	V	I	L	A	N	**I**	21
32	283	L	**V**	P	P	V	L	N	P	**I**	21
33	67	M	**L**	S	G	I	D	I	L	**I**	20
34	101	L	**Q**	I	F	A	I	H	S	**L**	20
35	282	L	**L**	V	P	P	V	L	N	**P**	20
36	299	E	**I**	R	Q	R	I	L	R	**L**	20
37	304	I	**L**	R	L	F	H	V	A	**T**	20
38	39	I	**A**	V	L	G	N	L	T	**I**	19
39	45	L	**T**	I	I	Y	I	V	R	**T**	19
40	92	T	**T**	I	Q	F	D	A	C	**L**	19
41	110	S	**G**	M	E	S	T	V	L	**L**	19
42	127	A	**I**	C	H	P	L	R	H	**A**	19
43	132	L	**R**	H	A	T	V	L	T	**L**	19
44	149	A	**A**	V	V	R	G	A	A	**L**	19
45	155	A	**A**	L	M	A	P	L	P	**V**	19
46	156	A	**L**	M	A	P	L	P	V	**F**	19
47	203	I	**V**	I	I	S	A	I	G	**L**	19
48	208	A	**I**	G	L	D	S	L	L	**I**	19
49	216	I	**S**	F	S	Y	L	L	I	**L**	19
50	219	S	**Y**	L	L	I	L	K	T	**V**	19
51	221	L	**L**	I	L	K	T	V	L	**G**	19
52	223	I	**L**	K	T	V	L	G	L	**T**	19
53	17	I	**G**	L	P	G	L	E	E	**A**	18
54	33	L	**C**	S	L	Y	L	I	A	**V**	18
55	34	C	**S**	L	Y	L	I	A	V	**L**	18
56	38	L	**I**	A	V	L	G	N	L	**T**	18
57	43	G	**N**	L	T	I	I	Y	I	**V**	18
58	85	A	**I**	F	W	F	N	S	T	**T**	18
59	118	L	**A**	M	A	F	D	R	Y	**V**	18
60	194	I	**R**	V	N	V	V	Y	G	**L**	18
61	210	G	**L**	D	S	L	L	I	S	**F**	18
62	215	L	**I**	S	F	S	Y	L	L	**I**	18
63	246	V	**C**	A	V	F	I	F	Y	**V**	18
64	254	V	**P**	F	I	G	L	S	M	**V**	18
65	15	I	**L**	I	G	L	P	G	L	**E**	17
66	63	I	**F**	L	C	M	L	S	G	**I**	17
67	72	D	**I**	L	I	S	T	S	S	**M**	17
68	93	T	**I**	Q	F	D	A	C	L	**L**	17
69	98	A	**C**	L	L	Q	I	F	A	**I**	17
70	111	G	**M**	E	S	T	V	L	L	**A**	17
71	120	M	**A**	F	D	R	Y	V	A	**I**	17
72	167	Q	**L**	P	F	C	R	S	N	**I**	17
73	197	N	**V**	V	Y	G	L	I	V	**I**	17
74	226	T	**V**	L	G	L	T	R	E	**A**	17
75	281	Y	**L**	L	V	P	P	V	L	**N**	17
76	31	F	**P**	L	C	S	L	Y	L	**I**	16

HLA-A*0201 nonomers (SEQ ID NOS 1463-1569, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
77	56	S	**L**	H	E	P	M	Y	I	**F**	16
78	70	G	**I**	D	I	L	I	S	T	**S**	16
79	78	S	**S**	M	P	K	M	L	A	**I**	16
80	79	S	**M**	P	K	M	L	A	I	**F**	16
81	104	F	**A**	I	H	S	L	S	G	**M**	16
82	119	A	**M**	A	F	D	R	Y	V	**A**	16
83	144	T	**K**	I	G	V	A	A	V	**V**	16
84	147	G	**V**	A	A	V	V	R	G	**A**	16
85	186	V	**M**	K	L	A	C	D	D	**I**	16
86	230	L	**T**	R	E	A	Q	A	K	**A**	16
87	238	A	**F**	G	T	C	V	S	H	**V**	16
88	249	V	**F**	I	F	Y	V	P	F	**I**	16
89	302	Q	**R**	I	L	R	L	F	H	**V**	16
90	303	R	**I**	L	R	L	F	H	V	**A**	16
91	18	G	**L**	P	G	L	E	E	A	**Q**	15
92	35	S	**L**	Y	L	I	A	V	L	**G**	15
93	42	L	**G**	N	L	T	I	I	Y	**I**	15
94	46	T	**I**	I	Y	I	V	R	T	**E**	15
95	69	S	**G**	I	D	I	L	I	S	**T**	15
96	76	S	**T**	S	S	M	P	K	M	**L**	15
97	131	P	**L**	R	H	A	T	V	L	**T**	15
98	137	V	**L**	T	L	P	R	V	T	**K**	15
99	153	R	**G**	A	A	L	M	A	P	**L**	15
100	190	A	**C**	D	D	I	R	V	N	**V**	15
101	191	C	**D**	D	I	R	V	N	V	**V**	15
102	204	V	**I**	I	S	A	I	G	L	**D**	15
103	241	T	**C**	V	S	H	V	C	A	**V**	15
104	251	I	**F**	Y	V	P	F	I	G	**L**	15
105	269	R	**D**	S	P	L	P	V	I	**L**	15
106	280	I	**Y**	L	L	V	P	P	V	**L**	15
107	306	R	**L**	F	H	V	A	T	H	**A**	15

HLA A*0203 nonomers (SEQ ID NOS 1570-1594, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	148	V	A	**A**	V	V	R	G	A	**A**	14
2	119	A	M	**A**	F	D	R	Y	V	**A**	13
3	147	G	V	**A**	A	V	V	R	G	**A**	12
4	97	D	A	**C**	L	L	Q	I	F	**A**	11
5	127	A	I	**C**	H	P	L	R	H	**A**	10
6	3	D	P	**N**	G	N	E	S	S	**A**	9
7	17	I	G	**L**	P	G	L	E	E	**A**	9
8	22	L	E	**E**	A	Q	F	W	L	**A**	9
9	32	P	L	**C**	S	L	Y	L	I	**A**	9
10	77	T	S	**S**	M	P	K	M	L	**A**	9
11	90	N	S	**T**	T	I	Q	F	D	**A**	9
12	111	G	M	**E**	S	T	V	L	L	**A**	9

HLA A*0203 nonomers (SEQ ID NOS 1570-1594, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
13	113	E	S	**T**	V	L	L	A	M	**A**	9
14	141	P	R	**V**	T	K	I	G	V	**A**	9
15	142	R	V	**T**	K	I	G	V	A	**A**	9
16	151	V	V	**R**	G	A	A	L	M	**A**	9
17	182	L	H	**Q**	D	V	M	K	L	**A**	9
18	200	Y	G	**L**	I	V	I	I	S	**A**	9
19	226	T	V	**L**	G	L	T	R	E	**A**	9
20	228	L	G	**L**	T	R	E	A	Q	**A**	9
21	230	L	T	**R**	E	A	Q	A	K	**A**	9
22	240	G	T	**C**	V	S	H	V	C	**A**	9
23	270	D	S	**P**	L	P	V	I	L	**A**	9
24	303	R	I	**L**	R	L	F	H	V	**A**	9
25	306	R	L	**F**	H	V	A	T	H	**A**	9

HLA-A26 nonomers (SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	R	Q	R	I	L	R	L	30
2	72	D	I	L	I	S	T	S	S	M	27
3	248	A	V	F	I	F	Y	V	P	F	27
4	210	G	L	D	S	L	L	I	S	F	26
5	14	F	I	L	I	G	L	P	G	L	24
6	56	S	L	H	E	P	M	Y	I	F	24
7	117	L	L	A	M	A	F	D	R	Y	24
8	222	L	I	L	K	T	V	L	G	L	24
9	245	H	V	C	A	V	F	I	F	Y	24
10	11	A	T	Y	F	I	L	I	G	L	23
11	37	Y	L	I	A	V	L	G	N	L	23
12	114	S	T	V	L	L	A	M	A	F	23
13	156	A	L	M	A	P	L	P	V	F	23
14	162	P	V	F	I	K	Q	L	P	F	23
15	181	C	L	H	Q	D	V	M	K	L	23
16	28	W	L	A	F	P	L	C	S	L	22
17	92	T	T	I	Q	F	D	A	C	L	22
18	160	P	L	P	V	F	I	K	Q	L	22
19	203	I	V	I	I	S	A	I	G	L	22
20	213	S	L	L	I	S	F	S	Y	L	22
21	275	V	I	L	A	N	I	Y	L	L	22
22	193	D	I	R	V	N	V	V	Y	G	21
23	242	C	V	S	H	V	C	A	V	F	21
24	76	S	T	S	S	M	P	K	M	L	20
25	253	Y	V	P	F	I	G	L	S	M	20
26	274	P	V	I	L	A	N	I	Y	L	20
27	23	E	E	A	Q	F	W	L	A	F	19
28	41	V	L	G	N	L	T	I	I	Y	19
29	49	Y	I	V	R	T	E	H	S	L	19
30	150	A	V	V	R	G	A	A	L	M	19

HLA-A26 nonomers (SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
31	174	N	I	L	S	H	S	Y	C	L	19
32	192	D	D	I	R	V	N	V	V	Y	19
33	214	L	L	I	S	F	S	Y	L	L	19
34	251	I	F	Y	V	P	F	I	G	L	19
35	8	E	S	S	A	T	Y	F	I	L	18
36	21	G	L	E	E	A	Q	F	W	L	18
37	45	L	T	I	I	Y	I	V	R	T	18
38	54	E	H	S	L	H	E	P	M	Y	18
39	59	E	P	M	Y	I	F	L	C	M	18
40	88	W	F	N	S	T	T	I	Q	F	18
41	93	T	I	Q	F	D	A	C	L	L	18
42	185	D	V	M	K	L	A	C	D	D	18
43	198	V	V	Y	G	L	I	V	I	I	18
44	62	Y	I	F	L	C	M	L	S	G	17
45	70	G	I	D	I	L	I	S	T	S	17
46	79	S	M	P	K	M	L	A	I	F	17
47	96	F	D	A	C	L	L	Q	I	F	17
48	104	F	A	I	H	S	L	S	G	M	17
49	138	L	T	L	P	R	V	T	K	I	17
50	143	V	T	K	I	G	V	A	A	V	17
51	204	V	I	I	S	A	I	G	L	D	17
52	212	D	S	L	L	I	S	F	S	Y	17
53	220	Y	L	L	I	L	K	T	V	L	17
54	256	F	I	G	L	S	M	V	H	R	17
55	283	L	V	P	P	V	L	N	P	I	17
56	29	L	A	F	P	L	C	S	L	Y	16
57	40	A	V	L	G	N	L	T	I	I	16
58	46	T	I	I	Y	I	V	R	T	E	16
59	52	R	T	E	H	S	L	H	E	P	16
60	75	I	S	T	S	S	M	P	K	M	16
61	91	S	T	T	I	Q	F	D	A	C	16
62	135	A	T	V	L	T	L	P	R	V	16
63	147	G	V	A	A	V	V	R	G	A	16
64	201	G	L	I	V	I	I	S	A	I	16
65	257	I	G	L	S	M	V	H	R	F	16
66	279	N	I	Y	L	L	V	P	P	V	16
67	30	A	F	P	L	C	S	L	Y	L	15
68	101	L	Q	I	F	A	I	H	S	L	15
69	115	T	V	L	L	A	M	A	F	D	15
70	127	A	I	C	H	P	L	R	H	A	15
71	153	R	G	A	A	L	M	A	P	L	15
72	163	V	F	I	K	Q	L	P	F	C	15
73	215	L	I	S	F	S	Y	L	L	I	15
74	216	I	S	F	S	Y	L	L	I	L	15
75	225	K	T	V	L	G	L	T	R	E	15
76	272	P	L	P	V	I	L	A	N	I	15
77	282	L	L	V	P	P	V	L	N	P	15
78	286	P	V	L	N	P	I	V	Y	G	15
79	287	V	L	N	P	I	V	Y	G	V	15

HLA-A26 nonomers (SEQ ID NOS 1595-1675, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
80	296	K	T	K	E	I	R	Q	R	I	15
81	303	R	I	L	R	L	F	H	V	A	15

HLA-A3 nonomers (SEQ ID NOS 1676-1747, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	137	V	**L**	T	L	P	R	V	T	**K**	30
2	229	G	**L**	T	R	E	A	Q	A	**K**	27
3	145	K	**I**	G	V	A	A	V	V	**R**	26
4	150	A	**V**	V	R	G	A	A	L	**M**	24
5	290	P	**I**	V	Y	G	V	K	T	**K**	24
6	35	S	**L**	Y	L	I	A	V	L	**G**	23
7	156	A	**L**	M	A	P	L	P	V	**F**	23
8	47	I	**I**	Y	I	V	R	T	E	**H**	22
9	50	I	**V**	R	T	E	H	S	L	**H**	22
10	142	R	**V**	T	K	I	G	V	A	**A**	22
11	151	V	**V**	R	G	A	A	L	M	**A**	22
12	242	C	**V**	S	H	V	C	A	V	**F**	22
13	248	A	**V**	F	I	F	Y	V	P	**F**	22
14	116	V	**L**	L	A	M	A	F	D	**R**	21
15	192	D	**D**	I	R	V	N	V	V	**Y**	21
16	303	R	**I**	L	R	L	F	H	V	**A**	21
17	304	I	**L**	R	L	F	H	V	A	**T**	21
18	108	S	**L**	S	G	M	E	S	T	**V**	20
19	198	V	**V**	Y	G	L	I	V	I	**I**	20
20	291	I	**V**	Y	G	V	K	T	K	**E**	20
21	15	I	**L**	I	G	L	P	G	L	**E**	19
22	44	N	**L**	T	I	I	Y	I	V	**R**	19
23	73	I	**L**	I	S	T	S	S	M	**P**	19
24	74	L	**I**	S	T	S	S	M	P	**K**	19
25	99	C	**L**	L	Q	I	F	A	I	**H**	19
26	162	P	**V**	F	I	K	Q	L	P	**F**	19
27	203	I	**V**	I	I	S	A	I	G	**L**	19
28	221	L	**L**	I	L	K	T	V	L	**G**	19
29	245	H	**V**	C	A	V	F	I	F	**Y**	19
30	306	R	**L**	F	H	V	A	T	H	**A**	19
31	40	A	**V**	L	G	N	L	T	I	**I**	18
32	85	A	**I**	F	W	F	N	S	T	**T**	18
33	205	I	**I**	S	A	I	G	L	D	**S**	18
34	220	Y	**L**	L	I	L	K	T	V	**L**	18
35	253	Y	**V**	P	F	I	G	L	S	**M**	18
36	37	Y	**L**	I	A	V	L	G	N	**L**	17
37	41	V	**L**	G	N	L	T	I	I	**Y**	17
38	117	L	**L**	A	M	A	F	D	R	**Y**	17
39	131	P	**L**	R	H	A	T	V	L	**T**	17
40	136	T	**V**	L	T	L	P	R	V	**T**	17
41	180	Y	**C**	L	H	Q	D	V	M	**K**	17

HLA-A3 nonomers(SEQ ID NOS 1676-1747, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
42	201	G	**L**	I	V	I	I	S	A	**I**	17
43	213	S	**L**	L	I	S	F	S	Y	**L**	17
44	256	F	**I**	G	L	S	M	V	H	**R**	17
45	261	M	**V**	H	R	F	S	K	R	**R**	17
46	276	I	**L**	A	N	I	Y	L	L	**V**	17
47	281	Y	**L**	L	V	P	P	V	L	**N**	17
48	286	P	**V**	L	N	P	I	V	Y	**G**	17
49	288	L	**N**	P	I	V	Y	G	V	**K**	17
50	309	H	**V**	A	T	H	A	S	E	**P**	17
51	1	M	**V**	D	P	N	G	N	E	**S**	16
52	56	S	**L**	H	E	P	M	Y	I	**F**	16
53	70	G	**I**	D	I	L	I	S	T	**S**	16
54	72	D	**I**	L	I	S	T	S	S	**M**	16
55	115	T	**V**	L	L	A	M	A	F	**D**	16
56	125	Y	**V**	A	I	C	H	P	L	**R**	16
57	144	T	**K**	I	G	V	A	A	V	**V**	16
58	167	Q	**L**	P	F	C	R	S	N	**I**	16
59	175	I	**L**	S	H	S	Y	C	L	**H**	16
60	195	R	**V**	N	V	V	Y	G	L	**I**	16
61	197	N	**V**	V	Y	G	L	I	V	**I**	16
62	210	G	**L**	D	S	L	L	I	S	**F**	16
63	282	L	**L**	V	P	P	V	L	N	**P**	16
64	299	E	**I**	R	Q	R	I	L	R	**L**	16
65	301	R	**Q**	R	I	L	R	L	F	**H**	16
66	16	L	**I**	G	L	P	G	L	E	**E**	15
67	46	T	**I**	I	Y	I	V	R	T	**E**	15
68	102	Q	**I**	F	A	I	H	S	L	**S**	15
69	193	D	**I**	R	V	N	V	V	Y	**G**	15
70	208	A	**I**	G	L	D	S	L	L	**I**	15
71	223	I	**L**	K	T	V	L	G	L	**T**	15
72	237	K	**A**	F	G	T	C	V	S	**H**	15

HLA-B*0702 nonomers(SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	130	H	**P**	L	R	H	A	T	V	**L**	22
2	59	E	**P**	M	Y	I	F	L	C	**M**	21
3	168	L	**P**	F	C	R	S	N	I	**L**	20
4	289	N	**P**	I	V	Y	G	V	K	**T**	19
5	3	D	**P**	N	G	N	E	S	S	**A**	18
6	19	L	**P**	G	L	E	E	A	Q	**F**	18
7	140	L	**P**	R	V	T	K	I	G	**V**	18
8	284	V	**P**	P	V	L	N	P	I	**V**	17
9	31	F	**P**	L	C	S	L	Y	L	**I**	16
10	254	V	**P**	F	I	G	L	S	M	**V**	16
11	269	R	**D**	S	P	L	P	V	I	**L**	16
12	149	A	**A**	V	V	R	G	A	A	**L**	15

HLA-B*0702 nonomers (SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
13	153	R	**G**	A	A	L	M	A	P	**L**	15
14	156	A	**L**	M	A	P	L	P	V	**F**	15
15	251	I	**F**	Y	V	P	F	I	G	**L**	15
16	299	E	**I**	R	Q	R	I	L	R	**L**	15
17	8	E	**S**	S	A	T	Y	F	I	**L**	14
18	28	W	**L**	A	F	P	L	C	S	**L**	14
19	30	A	**F**	P	L	C	S	L	Y	**L**	14
20	110	S	**G**	M	E	S	T	V	L	**L**	14
21	132	L	**R**	H	A	T	V	L	T	**L**	14
22	159	A	**P**	L	P	V	F	I	K	**Q**	14
23	222	L	**I**	L	K	T	V	L	G	**L**	14
24	271	S	**P**	L	P	V	I	L	A	**N**	14
25	25	A	**Q**	F	W	L	A	F	P	**L**	13
26	109	L	**S**	G	M	E	S	T	V	**L**	13
27	124	R	**Y**	V	A	I	C	H	P	**L**	13
28	216	I	**S**	F	S	Y	L	L	I	**L**	13
29	268	R	**R**	D	S	P	L	P	V	**I**	13
30	280	I	**Y**	L	L	V	P	P	V	**L**	13
31	11	A	**T**	Y	F	I	L	I	G	**L**	12
32	34	C	**S**	L	Y	L	I	A	V	**L**	12
33	57	L	**H**	E	P	M	Y	I	F	**L**	12
34	76	S	**T**	S	S	M	P	K	M	**L**	12
35	142	R	**V**	T	K	I	G	V	A	**A**	12
36	151	V	**V**	R	G	A	A	L	M	**A**	12
37	190	A	**C**	D	D	I	R	V	N	**V**	12
38	194	I	**R**	V	N	V	V	Y	G	**L**	12
39	206	I	**S**	A	I	G	L	D	S	**L**	12
40	207	S	**A**	I	G	L	D	S	L	**L**	12
41	220	Y	**L**	L	I	L	K	T	V	**L**	12
42	267	K	**R**	R	D	S	P	L	P	**V**	12
43	304	I	**L**	R	L	F	H	V	A	**T**	12
44	14	F	**I**	L	I	G	L	P	G	**L**	11
45	23	E	**E**	A	Q	F	W	L	A	**F**	11
46	37	Y	**L**	I	A	V	L	G	N	**L**	11
47	40	A	**V**	L	G	N	L	T	I	**I**	11
48	77	T	**S**	S	M	P	K	M	L	**A**	11
49	78	S	**S**	M	P	K	M	L	A	**I**	11
50	80	M	**P**	K	M	L	A	I	F	**W**	11
51	92	T	**T**	I	Q	F	D	A	C	**L**	11
52	112	M	**E**	S	T	V	L	L	A	**M**	11
53	119	A	**M**	A	F	D	R	Y	V	**A**	11
54	127	A	**I**	C	H	P	L	R	H	**A**	11
55	131	P	**L**	R	H	A	T	V	L	**T**	11
56	155	A	**A**	L	M	A	P	L	P	**V**	11
57	157	L	**M**	A	P	L	P	V	F	**I**	11
58	181	C	**L**	H	Q	D	V	M	K	**L**	11
59	203	I	**V**	I	I	S	A	I	G	**L**	11
60	208	A	**I**	G	L	D	S	L	L	**I**	11
61	213	S	**L**	L	I	S	F	S	Y	**L**	11

HLA-B*0702 nonomers (SEQ ID NOS 1748-1812, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
62	248	A	**V**	F	I	F	Y	V	P	**F**	11
63	265	F	**S**	K	R	R	D	S	P	**L**	11
64	275	V	**I**	L	A	N	I	Y	L	**L**	11
65	285	P	**P**	V	L	N	P	I	V	**Y**	11

HLA-B*08 nonomers (SEQ ID NOS 1813-1847, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	299	E	I	**R**	Q	**R**	I	L	R	**L**	31
2	265	F	S	**K**	R	**R**	D	S	P	**L**	29
3	149	A	A	**V**	V	**R**	G	A	A	**L**	24
4	168	L	P	**F**	C	**R**	S	N	I	**L**	24
5	294	G	V	**K**	T	**K**	E	I	R	**Q**	21
6	120	M	A	**F**	D	**R**	Y	V	A	**I**	20
7	292	V	Y	**G**	V	**K**	T	K	E	**I**	20
8	21	G	L	**E**	E	**A**	Q	F	W	**L**	19
9	78	S	S	**M**	P	**K**	M	L	A	**I**	19
10	160	P	L	**P**	V	**F**	I	K	Q	**L**	19
11	186	V	M	**K**	L	**A**	C	D	D	**I**	18
12	213	S	L	**L**	I	**S**	F	S	Y	**L**	18
13	221	L	L	**I**	L	**K**	T	V	L	**G**	18
14	296	K	T	**K**	E	**I**	R	Q	R	**I**	18
15	297	T	K	**E**	I	**R**	Q	R	I	**L**	18
16	130	H	P	**L**	R	**H**	A	T	V	**L**	17
17	181	C	L	**H**	Q	**D**	V	M	K	**L**	17
18	223	I	L	**K**	T	**V**	L	G	L	**T**	17
19	28	W	L	**A**	F	**P**	L	C	S	**L**	16
20	37	Y	L	**I**	A	**V**	L	G	N	**L**	16
21	56	S	L	**H**	E	**P**	M	Y	I	**F**	16
22	80	M	P	**K**	M	**L**	A	I	F	**W**	16
23	162	P	V	**F**	I	**K**	Q	L	P	**F**	16
24	201	G	L	**I**	V	**I**	I	S	A	**I**	16
25	207	S	A	**I**	G	**L**	D	S	L	**L**	16
26	214	L	L	**I**	S	**F**	S	Y	L	**L**	16
27	220	Y	L	**L**	I	**L**	K	T	V	**L**	16
28	233	E	A	**Q**	A	**K**	A	F	G	**T**	16
29	275	V	I	**L**	A	**N**	I	Y	L	**L**	16
30	304	I	L	**R**	L	**F**	H	V	A	**T**	16
31	14	F	I	**L**	I	**G**	L	P	G	**L**	15
32	110	S	G	**M**	E	**S**	T	V	L	**L**	15
33	138	L	T	**L**	P	**R**	V	T	K	**I**	15
34	164	F	I	**K**	Q	**L**	P	F	C	**R**	15
35	222	L	I	**L**	K	**T**	V	L	G	**L**	15

HLA-B*1510 nonomers (SEQ ID NOS 1848-1890, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	57	L	**H**	E	P	M	Y	I	F	**L**	23
2	244	S	**H**	V	C	A	V	F	I	**F**	17
3	269	R	**D**	S	P	L	P	V	I	**L**	16
4	280	I	**Y**	L	L	V	P	P	V	**L**	16
5	262	V	**H**	R	F	S	K	R	R	**D**	15
6	299	E	**I**	R	Q	R	I	L	R	**L**	15
7	106	I	**H**	S	L	S	G	M	E	**S**	14
8	206	I	**S**	A	I	G	L	D	S	**L**	14
9	220	Y	**L**	L	I	L	K	T	V	**L**	14
10	251	I	**F**	Y	V	P	F	I	G	**L**	14
11	297	T	**K**	E	I	R	Q	R	I	**L**	14
12	21	G	**L**	E	E	A	Q	F	W	**L**	13
13	34	C	**S**	L	Y	L	I	A	V	**L**	13
14	54	E	**H**	S	L	H	E	P	M	**Y**	13
15	110	S	**G**	M	E	S	T	V	L	**L**	13
16	194	I	**R**	V	N	V	V	Y	G	**L**	13
17	8	E	**S**	S	A	T	Y	F	I	**L**	12
18	14	F	**I**	L	I	G	L	P	G	**L**	12
19	28	W	**L**	A	F	P	L	C	S	**L**	12
20	66	C	**M**	L	S	G	I	D	I	**L**	12
21	76	S	**T**	S	S	M	P	K	M	**L**	12
22	92	T	**T**	I	Q	F	D	A	C	**L**	12
23	109	L	**S**	G	M	E	S	T	V	**L**	12
24	130	H	**P**	L	R	H	A	T	V	**L**	12
25	132	L	**R**	H	A	T	V	L	T	**L**	12
26	149	A	**A**	V	V	R	G	A	A	**L**	12
27	153	R	**G**	A	A	L	M	A	P	**L**	12
28	160	P	**L**	P	V	F	I	K	Q	**L**	12
29	181	C	**L**	H	Q	D	V	M	K	**L**	12
30	182	L	**H**	Q	D	V	M	K	L	**A**	12
31	203	I	**V**	I	I	S	A	I	G	**L**	12
32	216	I	**S**	F	S	Y	L	L	I	**L**	12
33	222	L	**I**	L	K	T	V	L	G	**L**	12
34	275	V	**I**	L	A	N	I	Y	L	**L**	12
35	37	Y	**L**	I	A	V	L	G	N	**L**	11
36	49	Y	**I**	V	R	T	E	H	S	**L**	11
37	93	T	**I**	Q	F	D	A	C	L	**L**	11
38	101	L	**Q**	I	F	A	I	H	S	**L**	11
39	129	C	**H**	P	L	R	H	A	T	**V**	11
40	133	R	**H**	A	T	V	L	T	L	**P**	11
41	177	S	**H**	S	Y	C	L	H	Q	**D**	11
42	207	S	**A**	I	G	L	D	S	L	**L**	11
43	257	I	**G**	L	S	M	V	H	R	**F**	11

HLA-B*2705 nonomers(SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	**R**	V	N	V	V	Y	G	**L**	25
2	268	R	**R**	D	S	P	L	P	V	**I**	24
3	132	L	**R**	H	A	T	V	L	T	**L**	23

HLA-B*2705 nonomers (SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
4	300	I	**R**	Q	R	I	L	R	L	**F**	23
5	305	L	**R**	L	F	H	V	A	T	**H**	23
6	231	T	**R**	E	A	Q	A	K	A	**F**	21
7	34	C	**S**	L	Y	L	I	A	V	**L**	18
8	299	E	**I**	R	Q	R	I	L	R	**L**	18
9	6	G	**N**	E	S	S	A	T	Y	**F**	17
10	66	C	**M**	L	S	G	I	D	I	**L**	17
11	162	P	**V**	F	I	K	Q	L	P	**F**	17
12	207	S	**A**	I	G	L	D	S	L	**L**	17
13	210	G	**L**	D	S	L	L	I	S	**F**	17
14	220	Y	**L**	L	I	L	K	T	V	**L**	17
15	237	K	**A**	F	G	T	C	V	S	**H**	17
16	269	R	**D**	S	P	L	P	V	I	**L**	17
17	280	I	**Y**	L	L	V	P	P	V	**L**	17
18	295	V	**K**	T	K	E	I	R	Q	**R**	17
19	11	A	**T**	Y	F	I	L	I	G	**L**	16
20	14	F	**I**	L	I	G	L	P	G	**L**	16
21	21	G	**L**	E	E	A	Q	F	W	**L**	16
22	25	A	**Q**	F	W	L	A	F	P	**L**	16
23	37	Y	**L**	I	A	V	L	G	N	**L**	16
24	92	T	**T**	I	Q	F	D	A	C	**L**	16
25	101	L	**Q**	I	F	A	I	H	S	**L**	16
26	124	R	**Y**	V	A	I	C	H	P	**L**	16
27	130	H	**P**	L	R	H	A	T	V	**L**	16
28	141	P	**R**	V	T	K	I	G	V	**A**	16
29	153	R	**G**	A	A	L	M	A	P	**L**	16
30	181	C	**L**	H	Q	D	V	M	K	**L**	16
31	201	G	**L**	I	V	I	I	S	A	**I**	16
32	203	I	**V**	I	I	S	A	I	G	**L**	16
33	216	I	**S**	F	S	Y	L	L	I	**L**	16
34	222	L	**I**	L	K	T	V	L	G	**L**	16
35	255	P	**F**	I	G	L	S	M	V	**H**	16
36	257	I	**G**	L	S	M	V	H	R	**F**	16
37	275	V	**I**	L	A	N	I	Y	L	**L**	16
38	47	I	**I**	Y	I	V	R	T	E	**H**	15
39	109	L	**S**	G	M	E	S	T	V	**L**	15
40	114	S	**T**	V	L	L	A	M	A	**F**	15
41	123	D	**R**	Y	V	A	I	C	H	**P**	15
42	145	K	**I**	G	V	A	A	V	V	**R**	15
43	156	A	**L**	M	A	P	L	P	V	**F**	15
44	168	L	**P**	F	C	R	S	N	I	**L**	15
45	172	R	**S**	N	I	L	S	H	S	**Y**	15
46	198	V	**V**	Y	G	L	I	V	I	**I**	15
47	206	I	**S**	A	I	G	L	D	S	**L**	15
48	229	G	**L**	T	R	E	A	Q	A	**K**	15
49	248	A	**V**	F	I	F	Y	V	P	**F**	15
50	251	I	**F**	Y	V	P	F	I	G	**L**	15
51	274	P	**V**	I	L	A	N	I	Y	**L**	15
52	290	P	**I**	V	Y	G	V	K	T	**K**	15

HLA-B*2705 nonomers (SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
53	298	K	**E**	I	R	Q	R	I	L	**R**	15
54	19	L	**P**	G	L	E	E	A	Q	**F**	14
55	29	L	**A**	F	P	L	C	S	L	**Y**	14
56	30	A	**F**	P	L	C	S	L	Y	**L**	14
57	39	I	**A**	V	L	G	N	L	T	**I**	14
58	40	A	**V**	L	G	N	L	T	I	**I**	14
59	79	S	**M**	P	K	M	L	A	I	**F**	14
60	81	P	**K**	M	L	A	I	F	W	**F**	14
61	99	C	**L**	L	Q	I	F	A	I	**H**	14
62	137	V	**L**	T	L	P	R	V	T	**K**	14
63	138	L	**T**	L	P	R	V	T	K	**I**	14
64	150	A	**V**	V	R	G	A	A	L	**M**	14
65	160	P	**L**	P	V	F	I	K	Q	**L**	14
66	174	N	**I**	L	S	H	S	Y	C	**L**	14
67	180	Y	**C**	L	H	Q	D	V	M	**K**	14
68	192	D	**D**	I	R	V	N	V	V	**Y**	14
69	212	D	**S**	L	L	I	S	F	S	**Y**	14
70	213	S	**L**	L	I	S	F	S	Y	**L**	14
71	214	L	**L**	I	S	F	S	Y	L	**L**	14
72	260	S	**M**	V	H	R	F	S	K	**R**	14
73	263	H	**R**	F	S	K	R	R	D	**S**	14
74	267	K	**R**	R	D	S	P	L	P	**V**	14
75	293	Y	**G**	V	K	T	K	E	I	**R**	14
76	301	R	**Q**	R	I	L	R	L	F	**H**	14
77	302	Q	**R**	I	L	R	L	F	H	**V**	14
78	5	N	**G**	N	E	S	S	A	T	**Y**	13
79	23	E	**E**	A	Q	F	W	L	A	**F**	13
80	28	W	**L**	A	F	P	L	C	S	**L**	13
81	44	N	**L**	T	I	I	Y	I	V	**R**	13
82	51	V	**R**	T	E	H	S	L	H	**E**	13
83	56	S	**L**	H	E	P	M	Y	I	**F**	13
84	60	P	**M**	Y	I	F	L	C	M	**L**	13
85	72	D	**I**	L	I	S	T	S	S	**M**	13
86	74	L	**I**	S	T	S	S	M	P	**K**	13
87	75	I	**S**	T	S	S	M	P	K	**M**	13
88	98	A	**C**	L	L	Q	I	F	A	**I**	13
89	104	F	**A**	I	H	S	L	S	G	**M**	13
90	110	S	**G**	M	E	S	T	V	L	**L**	13
91	116	V	**L**	L	A	M	A	F	D	**R**	13
92	126	V	**A**	I	C	H	P	L	R	**H**	13
93	149	A	**A**	V	V	R	G	A	A	**L**	13
94	158	M	**A**	P	L	P	V	F	I	**K**	13
95	164	F	**I**	K	Q	L	P	F	C	**R**	13
96	170	F	**C**	R	S	N	I	L	S	**H**	13
97	171	C	**R**	S	N	I	L	S	H	**S**	13
98	187	M	**K**	L	A	C	D	D	I	**R**	13
99	217	S	**F**	S	Y	L	L	I	L	**K**	13
100	224	L	**K**	T	V	L	G	L	T	**R**	13
101	242	C	**V**	S	H	V	C	A	V	**F**	13

HLA-B*2705 nonomers (SEQ ID NOS 1891-2008, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
102	256	F	**I**	G	L	S	M	V	H	**R**	13
103	261	M	**V**	H	R	F	S	K	R	**R**	13
104	49	Y	**I**	V	R	T	E	H	S	**L**	12
105	57	L	**H**	E	P	M	Y	I	F	**L**	12
106	88	W	**F**	N	S	T	T	I	Q	**F**	12
107	96	F	**D**	A	C	L	L	Q	I	**F**	12
108	134	H	**A**	T	V	L	T	L	P	**R**	12
109	152	V	**R**	G	A	A	L	M	A	**P**	12
110	179	S	**Y**	C	L	H	Q	D	V	**M**	12
111	197	N	**V**	V	Y	G	L	I	V	**I**	12
112	244	S	**H**	V	C	A	V	F	I	**F**	12
113	265	F	**S**	K	R	R	D	S	P	**L**	12
114	273	L	**P**	V	I	L	A	N	I	**Y**	12
115	285	P	**P**	V	L	N	P	I	V	**Y**	12
116	288	L	**N**	P	I	V	Y	G	V	**K**	12
117	296	K	**T**	K	E	I	R	Q	R	**I**	12
118	297	T	**K**	E	I	R	Q	R	I	**L**	12

HLA-B*2709 nonomers (SEQ ID NOS 2009-2063, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	194	I	R	V	N	V	V	Y	G	L	24
2	268	R	R	D	S	P	L	P	V	I	24
3	132	L	R	H	A	T	V	L	T	L	22
4	267	K	R	R	D	S	P	L	P	V	21
5	300	I	R	Q	R	I	L	R	L	F	20
6	231	T	R	E	A	Q	A	K	A	F	19
7	302	Q	R	I	L	R	L	F	H	V	19
8	124	R	Y	V	A	I	C	H	P	L	16
9	269	R	D	S	P	L	P	V	I	L	16
10	43	G	N	L	T	I	I	Y	I	V	15
11	216	I	S	F	S	Y	L	L	I	L	15
12	11	A	T	Y	F	I	L	I	G	L	14
13	25	A	Q	F	W	L	A	F	P	L	14
14	153	R	G	A	A	L	M	A	P	L	14
15	174	N	I	L	S	H	S	Y	C	L	14
16	222	L	I	L	K	T	V	L	G	L	14
17	257	I	G	L	S	M	V	H	R	F	14
18	280	I	Y	L	L	V	P	P	V	L	14
19	6	G	N	E	S	S	A	T	Y	F	13
20	14	F	I	L	I	G	L	P	G	L	13
21	21	G	L	E	E	A	Q	F	W	L	13
22	66	C	M	L	S	G	I	D	I	L	13
23	130	H	P	L	R	H	A	T	V	L	13
24	201	G	L	I	V	I	I	S	A	I	13
25	203	I	V	I	I	S	A	I	G	L	13

HLA-B*2709 nonomers (SEQ ID NOS 2009-2063, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
26	214	L	L	I	S	F	S	Y	L	L	13
27	251	I	F	Y	V	P	F	I	G	L	13
28	263	H	R	F	S	K	R	R	D	S	13
29	275	V	I	L	A	N	I	Y	L	L	13
30	305	L	R	L	F	H	V	A	T	H	13
31	30	A	F	P	L	C	S	L	Y	L	12
32	34	C	S	L	Y	L	I	A	V	L	12
33	37	Y	L	I	A	V	L	G	N	L	12
34	51	V	R	T	E	H	S	L	H	E	12
35	60	P	M	Y	I	F	L	C	M	L	12
36	75	I	S	T	S	S	M	P	K	M	12
37	93	T	I	Q	F	D	A	C	L	L	12
38	123	D	R	Y	V	A	I	C	H	P	12
39	135	A	T	V	L	T	L	P	R	V	12
40	138	L	T	L	P	R	V	T	K	I	12
41	149	A	A	V	V	R	G	A	A	L	12
42	155	A	A	L	M	A	P	L	P	V	12
43	168	L	P	F	C	R	S	N	I	L	12
44	181	C	L	H	Q	D	V	M	K	L	12
45	188	K	L	A	C	D	D	I	R	V	12
46	190	A	C	D	D	I	R	V	N	V	12
47	195	R	V	N	V	V	Y	G	L	I	12
48	210	G	L	D	S	L	L	I	S	F	12
49	213	S	L	L	I	S	F	S	Y	L	12
50	220	Y	L	L	I	L	K	T	V	L	12
51	248	A	V	F	I	F	Y	V	P	F	12
52	279	N	I	Y	L	L	V	P	P	V	12
53	287	V	L	N	P	I	V	Y	G	V	12
54	296	K	T	K	E	I	R	Q	R	I	12
55	299	E	I	R	Q	R	I	L	R	L	12

HLA-B*5101 nonomers (SEQ ID NOS 2064-2132, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
1	39	I	**A**	V	L	G	N	L	T	**I**	26
2	31	F	**P**	L	C	S	L	Y	L	**I**	25
3	120	M	**A**	F	D	R	Y	V	A	**I**	24
4	130	H	**P**	L	R	H	A	T	V	**L**	23
5	118	L	**A**	M	A	F	D	R	Y	**V**	22
6	140	L	**P**	R	V	T	K	I	G	**V**	22
7	155	A	**A**	L	M	A	P	L	P	**V**	22
8	42	L	**G**	N	L	T	I	I	Y	**I**	21
9	254	V	**P**	F	I	G	L	S	M	**V**	21
10	284	V	**P**	P	V	L	N	P	I	**V**	21
11	168	L	**P**	F	C	R	S	N	I	**L**	20
12	235	Q	**A**	K	A	F	G	T	C	**V**	20
13	138	L	**T**	L	P	R	V	T	K	**I**	19

HLA-B*5101 nonomers (SEQ ID NOS 2064-2132, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
14	159	A	**P**	L	P	V	F	I	K	**Q**	18
15	189	L	**A**	C	D	D	I	R	V	**N**	18
16	198	V	**V**	Y	G	L	I	V	I	**I**	18
17	277	L	**A**	N	I	Y	L	L	V	**P**	18
18	207	S	**A**	I	G	L	D	S	L	**L**	17
19	283	L	**V**	P	P	V	L	N	P	**I**	17
20	63	I	**F**	L	C	M	L	S	G	**I**	16
21	86	I	**F**	W	F	N	S	T	T	**I**	16
22	110	S	**G**	M	E	S	T	V	L	**L**	16
23	144	T	**K**	I	G	V	A	A	V	**V**	16
24	149	A	**A**	V	V	R	G	A	A	**L**	16
25	197	N	**V**	V	Y	G	L	I	V	**I**	16
26	271	S	**P**	L	P	V	I	L	A	**N**	16
27	280	I	**Y**	L	L	V	P	P	V	**L**	16
28	3	D	**P**	N	G	N	E	S	S	**A**	15
29	40	A	**V**	L	G	N	L	T	I	**I**	15
30	97	D	**A**	C	L	L	Q	I	F	**A**	15
31	132	L	**R**	H	A	T	V	L	T	**L**	15
32	222	L	**I**	L	K	T	V	L	G	**L**	15
33	279	N	**I**	Y	L	L	V	P	P	**V**	15
34	285	P	**P**	V	L	N	P	I	V	**Y**	15
35	289	N	**P**	I	V	Y	G	V	K	**T**	15
36	9	S	**S**	A	T	Y	F	I	L	**I**	14
37	65	L	**C**	M	L	S	G	I	D	**I**	14
38	84	L	**A**	I	F	W	F	N	S	**T**	14
39	126	V	**A**	I	C	H	P	L	R	**H**	14
40	157	L	**M**	A	P	L	P	V	F	**I**	14
41	158	M	**A**	P	L	P	V	F	I	**K**	14
42	191	C	**D**	D	I	R	V	N	V	**V**	14
43	200	Y	**G**	L	I	V	I	I	S	**A**	14
44	209	I	**G**	L	D	S	L	L	I	**S**	14
45	215	L	**I**	S	F	S	Y	L	L	**I**	14
46	219	S	**Y**	L	L	I	L	K	T	**V**	14
47	220	Y	**L**	L	I	L	K	T	V	**L**	14
48	237	K	**A**	F	G	T	C	V	S	**H**	14
49	247	C	**A**	V	F	I	F	Y	V	**P**	14
50	249	V	**F**	I	F	Y	V	P	F	**I**	14
51	251	I	**F**	Y	V	P	F	I	G	**L**	14
52	257	I	**G**	L	S	M	V	H	R	**F**	14
53	268	R	**R**	D	S	P	L	P	V	**I**	14
54	273	L	**P**	V	I	L	A	N	I	**Y**	14
55	29	L	**A**	F	P	L	C	S	L	**Y**	13
56	33	L	**C**	S	L	Y	L	I	A	**V**	13
57	55	H	**S**	L	H	E	P	M	Y	**I**	13
58	67	M	**L**	S	G	I	D	I	L	**I**	13
59	80	M	**P**	K	M	L	A	I	F	**W**	13
60	95	Q	**F**	D	A	C	L	L	Q	**I**	13
61	98	A	**C**	L	L	Q	I	F	A	**I**	13
62	104	F	**A**	I	H	S	L	S	G	**M**	13

HLA-B*5101 nonomers (SEQ ID NOS 2064-2132, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	score
63	146	I	**G**	V	A	A	V	V	R	**G**	13
64	148	V	**A**	A	V	V	R	G	A	**A**	13
65	153	R	**G**	A	A	L	M	A	P	**L**	13
66	233	E	**A**	Q	A	K	A	F	G	**T**	13
67	243	V	**S**	H	V	C	A	V	F	**I**	13
68	292	V	**Y**	G	V	K	T	K	E	**I**	13
69	296	K	**T**	K	E	I	R	Q	R	**I**	13

Table XXVII, beginning at page 201, line 1, has been amended as follows:

Table XXVII:
HLA Class I decamers

HLA-A1 decamers (SEQ ID NOS 2133-2153, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	191	C	D	**D**	I	R	V	N	V	**V**	Y	27
2	244	S	H	**V**	C	A	V	F	I	**F**	Y	24
3	40	A	V	**L**	G	N	L	T	I	**I**	Y	21
4	284	V	P	**P**	V	L	N	P	I	**V**	Y	21
5	116	V	L	**L**	A	M	A	F	D	**R**	Y	20
6	28	W	L	**A**	F	P	L	C	S	**L**	Y	18
7	297	T	K	**E**	I	R	Q	R	I	**L**	R	17
8	21	G	L	**E**	E	A	Q	F	W	**L**	A	16
9	22	L	E	**E**	A	Q	F	W	L	**A**	F	16
10	52	R	T	**E**	H	S	L	H	E	**P**	M	16
11	53	T	E	**H**	S	L	H	E	P	**M**	Y	16
12	57	L	H	**E**	P	M	Y	I	F	**L**	C	16
13	111	G	M	**E**	S	T	V	L	L	**A**	M	16
14	272	P	L	**P**	V	I	L	A	N	**I**	Y	16
15	1	M	V	**D**	P	N	G	N	E	**S**	S	15
16	4	P	N	**G**	N	E	S	S	A	**T**	Y	15
17	121	A	F	**D**	R	Y	V	A	I	**C**	H	15
18	171	C	R	**S**	N	I	L	S	H	**S**	Y	15
19	211	L	D	**S**	L	L	I	S	F	**S**	Y	15
20	8	E	S	**S**	A	T	Y	F	I	**L**	I	13
21	190	A	C	**D**	D	I	R	V	N	**V**	V	13

HLA-A*0201 decamers (SEQ ID NOS 2154-2253, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	221	L	**L**	I	L	K	T	V	L	**G**	L	30
2	100	L	**L**	Q	I	F	A	I	H	**S**	L	29
3	282	L	**L**	V	P	P	V	L	N	**P**	I	27
4	205	I	**I**	S	A	I	G	L	D	**S**	L	26
5	213	S	**L**	L	I	S	F	S	Y	**L**	L	25

HLA-A*0201 decamers (SEQ ID NOS 2154-2253, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
6	56	S	**L**	H	E	P	M	Y	I	**F**	L	24
7	62	Y	**I**	F	L	C	M	L	S	**G**	I	24
8	108	S	**L**	S	G	M	E	S	T	**V**	L	24
9	117	L	**L**	A	M	A	F	D	R	**Y**	V	24
10	131	P	**L**	R	H	A	T	V	L	**T**	L	24
11	137	V	**L**	T	L	P	R	V	T	**K**	I	24
12	215	L	**I**	S	F	S	Y	L	L	**I**	L	24
13	38	L	**I**	A	V	L	G	N	L	**T**	I	23
14	41	V	**L**	G	N	L	T	I	I	**Y**	I	23
15	156	A	**L**	M	A	P	L	P	V	**F**	I	23
16	193	D	**I**	R	V	N	V	V	Y	**G**	L	23
17	214	L	**L**	I	S	F	S	Y	L	**L**	I	23
18	32	P	**L**	C	S	L	Y	L	I	**A**	V	22
19	119	A	**M**	A	F	D	R	Y	V	**A**	I	22
20	237	K	**A**	F	G	T	C	V	S	**H**	V	22
21	275	V	**I**	L	A	N	I	Y	L	**L**	V	22
22	85	A	**I**	F	W	F	N	S	T	**T**	I	21
23	139	T	**L**	P	R	V	T	K	I	**G**	V	21
24	202	L	**I**	V	I	I	S	A	I	**G**	L	21
25	13	Y	**F**	I	L	I	G	L	P	**G**	L	20
26	16	L	**I**	G	L	P	G	L	E	**E**	A	20
27	29	L	**A**	F	P	L	C	S	L	**Y**	L	20
28	142	R	**V**	T	K	I	G	V	A	**A**	V	20
29	148	V	**A**	A	V	V	R	G	A	**A**	L	20
30	167	Q	**L**	P	F	C	R	S	N	**I**	L	20
31	180	Y	**C**	L	H	Q	D	V	M	**K**	L	20
32	222	L	**I**	L	K	T	V	L	G	**L**	T	20
33	240	G	**T**	C	V	S	H	V	C	**A**	V	20
34	248	A	**V**	F	I	F	Y	V	P	**F**	I	20
35	250	F	**I**	F	Y	V	P	F	I	**G**	L	20
36	271	S	**P**	L	P	V	I	L	A	**N**	I	20
37	279	N	**I**	Y	L	L	V	P	P	**V**	L	20
38	304	I	**L**	R	L	F	H	V	A	**T**	H	20
39	10	S	**A**	T	Y	F	I	L	I	**G**	L	19
40	15	I	**L**	I	G	L	P	G	L	**E**	E	19
41	27	F	**W**	L	A	F	P	L	C	**S**	L	19
42	35	S	**L**	Y	L	I	A	V	L	**G**	N	19
43	37	Y	**L**	I	A	V	L	G	N	**L**	T	19
44	44	N	**L**	T	I	I	Y	I	V	**R**	T	19
45	64	F	**L**	C	M	L	S	G	I	**D**	I	19
46	83	M	**L**	A	I	F	W	F	N	**S**	T	19
47	159	A	**P**	L	P	V	F	I	K	**Q**	L	19
48	189	L	**A**	C	D	D	I	R	V	**N**	V	19
49	207	S	**A**	I	G	L	D	S	L	**L**	I	19
50	253	Y	**V**	P	F	I	G	L	S	**M**	V	19
51	276	I	**L**	A	N	I	Y	L	L	**V**	P	19
52	281	Y	**L**	L	V	P	P	V	L	**N**	P	19
53	283	L	**V**	P	P	V	L	N	P	**I**	V	19
54	286	P	**V**	L	N	P	I	V	Y	**G**	V	19
55	33	L	**C**	S	L	Y	L	I	A	**V**	L	18

HLA-A*0201 decamers (SEQ ID NOS 2154-2253, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
56	36	L	**Y**	L	I	A	V	L	G	**N**	L	18
57	39	I	**A**	V	L	G	N	L	T	**I**	I	18
58	42	L	**G**	N	L	T	I	I	Y	**I**	V	18
59	66	C	**M**	L	S	G	I	D	I	**L**	I	18
60	111	G	**M**	E	S	T	V	L	L	**A**	M	18
61	128	I	**C**	H	P	L	R	H	A	**T**	V	18
62	134	H	**A**	T	V	L	T	L	P	**R**	V	18
63	154	G	**A**	A	L	M	A	P	L	**P**	V	18
64	157	L	**M**	A	P	L	P	V	F	**I**	K	18
65	190	A	**C**	D	D	I	R	V	N	**V**	V	18
66	229	G	**L**	T	R	E	A	Q	A	**K**	A	18
67	245	H	**V**	C	A	V	F	I	F	**Y**	V	18
68	274	P	**V**	I	L	A	N	I	Y	**L**	L	18
69	278	A	**N**	I	Y	L	L	V	P	**P**	V	18
70	291	I	**V**	Y	G	V	K	T	K	**E**	I	18
71	298	K	**E**	I	R	Q	R	I	L	**R**	L	18
72	48	I	**Y**	I	V	R	T	E	H	**S**	L	17
73	65	L	**C**	M	L	S	G	I	D	**I**	L	17
74	67	M	**L**	S	G	I	D	I	L	**I**	S	17
75	74	L	**I**	S	T	S	S	M	P	**K**	M	17
76	91	S	**T**	T	I	Q	F	D	A	**C**	L	17
77	94	I	**Q**	F	D	A	C	L	L	**Q**	I	17
78	188	K	**L**	A	C	D	D	I	R	**V**	N	17
79	197	N	**V**	V	Y	G	L	I	V	**I**	I	17
80	200	Y	**G**	L	I	V	I	I	S	**A**	I	17
81	218	F	**S**	Y	L	L	I	L	K	**T**	V	17
82	227	V	**L**	G	L	T	R	E	A	**Q**	A	17
83	303	R	**I**	L	R	L	F	H	V	**A**	T	17
84	21	G	**L**	E	E	A	Q	F	W	**L**	A	16
85	92	T	**T**	I	Q	F	D	A	C	**L**	L	16
86	97	D	**A**	C	L	L	Q	I	F	**A**	I	16
87	127	A	**I**	C	H	P	L	R	H	**A**	T	16
88	143	V	**T**	K	I	G	V	A	A	**V**	V	16
89	195	R	**V**	N	V	V	Y	G	L	**I**	V	16
90	220	Y	**L**	L	I	L	K	T	V	**L**	G	16
91	296	K	**T**	K	E	I	R	Q	R	**I**	L	16
92	18	G	**L**	P	G	L	E	E	A	**Q**	F	15
93	30	A	**F**	P	L	C	S	L	Y	**L**	I	15
94	126	V	**A**	I	C	H	P	L	R	**H**	A	15
95	145	K	**I**	G	V	A	A	V	V	**R**	G	15
96	173	S	**N**	I	L	S	H	S	Y	**C**	L	15
97	201	G	**L**	I	V	I	I	S	A	**I**	G	15
98	208	A	**I**	G	L	D	S	L	L	**I**	S	15
99	210	G	**L**	D	S	L	L	I	S	**F**	S	15
100	267	K	**R**	R	D	S	P	L	P	**V**	I	15

HLA-A*0203 decamers (SEQ ID NOS 2254-2301, respectively in order of appearance)

Pos	1	2	3	4	5	6	7	8	9	0	score

HLA-A*0203 decamers (SEQ ID NOS 2254-2301, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	141	P	R	**V**	T	K	I	G	V	**A**	A	19
2	147	G	V	**A**	A	V	V	R	G	**A**	A	19
3	112	M	E	**S**	T	V	L	L	A	**M**	A	18
4	227	V	L	**G**	L	T	R	E	A	**Q**	A	18
5	229	G	L	**T**	R	E	A	Q	A	**K**	A	18
6	142	R	V	**T**	K	I	G	V	A	**A**	V	17
7	148	V	A	**A**	V	V	R	G	A	**A**	L	17
8	2	V	D	**P**	N	G	N	E	S	**S**	A	10
9	16	L	I	**G**	L	P	G	L	E	**E**	A	10
10	21	G	L	**E**	E	A	Q	F	W	**L**	A	10
11	31	F	P	**L**	C	S	L	Y	L	**I**	A	10
12	76	S	T	**S**	S	M	P	K	M	**L**	A	10
13	89	F	N	**S**	T	T	I	Q	F	**D**	A	10
14	96	F	D	**A**	C	L	L	Q	I	**F**	A	10
15	110	S	G	**M**	E	S	T	V	L	**L**	A	10
16	118	L	A	**M**	A	F	D	R	Y	**V**	A	10
17	126	V	A	**I**	C	H	P	L	R	**H**	A	10
18	140	L	P	**R**	V	T	K	I	G	**V**	A	10
19	146	I	G	**V**	A	A	V	V	R	**G**	A	10
20	150	A	V	**V**	R	G	A	A	L	**M**	A	10
21	181	C	L	**H**	Q	D	V	M	K	**L**	A	10
22	199	V	Y	**G**	L	I	V	I	I	**S**	A	10
23	225	K	T	**V**	L	G	L	T	R	**E**	A	10
24	239	F	G	**T**	C	V	S	H	V	**C**	A	10
25	269	R	D	**S**	P	L	P	V	I	**L**	A	10
26	302	Q	R	**I**	L	R	L	F	H	**V**	A	10
27	305	L	R	**L**	F	H	V	A	T	**H**	A	10
28	3	D	P	**N**	G	N	E	S	S	**A**	T	9
29	17	I	G	**L**	P	G	L	E	E	**A**	Q	9
30	22	L	E	**E**	A	Q	F	W	L	**A**	F	9
31	32	P	L	**C**	S	L	Y	L	I	**A**	V	9
32	77	T	S	**S**	M	P	K	M	L	**A**	I	9
33	90	N	S	**T**	T	I	Q	F	D	**A**	C	9
34	97	D	A	**C**	L	L	Q	I	F	**A**	I	9
35	111	G	M	**E**	S	T	V	L	L	**A**	M	9
36	113	E	S	**T**	V	L	L	A	M	**A**	F	9
37	119	A	M	**A**	F	D	R	Y	V	**A**	I	9
38	127	A	I	**C**	H	P	L	R	H	**A**	T	9
39	151	V	V	**R**	G	A	A	L	M	**A**	P	9
40	182	L	H	**Q**	D	V	M	K	L	**A**	C	9
41	200	Y	G	**L**	I	V	I	I	S	**A**	I	9
42	226	T	V	**L**	G	L	T	R	E	**A**	Q	9
43	228	L	G	**L**	T	R	E	A	Q	**A**	K	9
44	230	L	T	**R**	E	A	Q	A	K	**A**	F	9
45	240	G	T	**C**	V	S	H	V	C	**A**	V	9
46	270	D	S	**P**	L	P	V	I	L	**A**	N	9
47	303	R	I	**L**	R	L	F	H	V	**A**	T	9
48	306	R	L	**F**	H	V	A	T	H	**A**	S	9

HLA-A26 decamers (SEQ ID NOS 2302-2366, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	299	E	I	R	Q	R	I	L	R	L	F	31
2	193	D	I	R	V	N	V	V	Y	G	L	29
3	250	F	I	F	Y	V	P	F	I	G	L	25
4	256	F	I	G	L	S	M	V	H	R	F	25
5	74	L	I	S	T	S	S	M	P	K	M	24
6	274	P	V	I	L	A	N	I	Y	L	L	24
7	18	G	L	P	G	L	E	E	A	Q	F	23
8	116	V	L	L	A	M	A	F	D	R	Y	23
9	205	I	I	S	A	I	G	L	D	S	L	23
10	221	L	L	I	L	K	T	V	L	G	L	23
11	230	L	T	R	E	A	Q	A	K	A	F	23
12	13	Y	F	I	L	I	G	L	P	G	L	22
13	40	A	V	L	G	N	L	T	I	I	Y	22
14	56	S	L	H	E	P	M	Y	I	F	L	22
15	95	Q	F	D	A	C	L	L	Q	I	F	22
16	215	L	I	S	F	S	Y	L	L	I	L	22
17	92	T	T	I	Q	F	D	A	C	L	L	21
18	100	L	L	Q	I	F	A	I	H	S	L	21
19	103	I	F	A	I	H	S	L	S	G	M	21
20	296	K	T	K	E	I	R	Q	R	I	L	21
21	28	W	L	A	F	P	L	C	S	L	Y	20
22	131	P	L	R	H	A	T	V	L	T	L	20
23	59	E	P	M	Y	I	F	L	C	M	L	19
24	91	S	T	T	I	Q	F	D	A	C	L	19
25	202	L	I	V	I	I	S	A	I	G	L	19
26	212	D	S	L	L	I	S	F	S	Y	L	19
27	272	P	L	P	V	I	L	A	N	I	Y	19
28	279	N	I	Y	L	L	V	P	P	V	L	19
29	52	R	T	E	H	S	L	H	E	P	M	18
30	62	Y	I	F	L	C	M	L	S	G	I	18
31	72	D	I	L	I	S	T	S	S	M	P	18
32	108	S	L	S	G	M	E	S	T	V	L	18
33	113	E	S	T	V	L	L	A	M	A	F	18
34	151	V	V	R	G	A	A	L	M	A	P	18
35	78	S	S	M	P	K	M	L	A	I	F	17
36	142	R	V	T	K	I	G	V	A	A	V	17
37	162	P	V	F	I	K	Q	L	P	F	C	17
38	164	F	I	K	Q	L	P	F	C	R	S	17
39	167	Q	L	P	F	C	R	S	N	I	L	17
40	185	D	V	M	K	L	A	C	D	D	I	17
41	248	A	V	F	I	F	Y	V	P	F	I	17
42	253	Y	V	P	F	I	G	L	S	M	V	17
43	45	L	T	I	I	Y	I	V	R	T	E	16
44	145	K	I	G	V	A	A	V	V	R	G	16
45	198	V	V	Y	G	L	I	V	I	I	S	16
46	203	I	V	I	I	S	A	I	G	L	D	16
47	209	I	G	L	D	S	L	L	I	S	F	16
48	213	S	L	L	I	S	F	S	Y	L	L	16
49	255	P	F	I	G	L	S	M	V	H	R	16
50	264	R	F	S	K	R	R	D	S	P	L	16

HLA-A26 decamers (SEQ ID NOS 2302-2366, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
51	294	G	V	K	T	K	E	I	R	Q	R	16
52	16	L	I	G	L	P	G	L	E	E	A	15
53	80	M	P	K	M	L	A	I	F	W	F	15
54	114	S	T	V	L	L	A	M	A	F	D	15
55	155	A	A	L	M	A	P	L	P	V	F	15
56	159	A	P	L	P	V	F	I	K	Q	L	15
57	174	N	I	L	S	H	S	Y	C	L	H	15
58	197	N	V	V	Y	G	L	I	V	I	I	15
59	210	G	L	D	S	L	L	I	S	F	S	15
60	214	L	L	I	S	F	S	Y	L	L	I	15
61	222	L	I	L	K	T	V	L	G	L	T	15
62	240	G	T	C	V	S	H	V	C	A	V	15
63	247	C	A	V	F	I	F	Y	V	P	F	15
64	286	P	V	L	N	P	I	V	Y	G	V	15
65	298	K	E	I	R	Q	R	I	L	R	L	15

HLA-A3 decamers (SEQ ID NOS 2367-2432, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	136	T	**V**	L	T	L	P	R	V	**T**	K	31
2	287	V	**L**	N	P	I	V	Y	G	**V**	K	28
3	223	I	**L**	K	T	V	L	G	L	**T**	R	27
4	304	I	**L**	R	L	F	H	V	A	**T**	H	27
5	73	I	**L**	I	S	T	S	S	M	**P**	K	26
6	15	I	**L**	I	G	L	P	G	L	**E**	E	23
7	40	A	**V**	L	G	N	L	T	I	**I**	Y	23
8	150	A	**V**	V	R	G	A	A	L	**M**	A	23
9	258	G	**L**	S	M	V	H	R	F	**S**	K	23
10	18	G	**L**	P	G	L	E	E	A	**Q**	F	22
11	303	R	**I**	L	R	L	F	H	V	**A**	T	22
12	276	I	**L**	A	N	I	Y	L	L	**V**	P	21
13	28	W	**L**	A	F	P	L	C	S	**L**	Y	20
14	115	T	**V**	L	L	A	M	A	F	**D**	R	20
15	116	V	**L**	L	A	M	A	F	D	**R**	Y	20
16	125	Y	**V**	A	I	C	H	P	L	**R**	H	20
17	131	P	**L**	R	H	A	T	V	L	**T**	L	20
18	144	T	**K**	I	G	V	A	A	V	**V**	R	20
19	156	A	**L**	M	A	P	L	P	V	**F**	I	20
20	195	R	**V**	N	V	V	Y	G	L	**I**	V	20
21	35	S	**L**	Y	L	I	A	V	L	**G**	N	19
22	272	P	**L**	P	V	I	L	A	N	**I**	Y	19
23	37	Y	**L**	I	A	V	L	G	N	**L**	T	18
24	49	Y	**I**	V	R	T	E	H	S	**L**	H	18
25	50	I	**V**	R	T	E	H	S	L	**H**	E	18
26	108	S	**L**	S	G	M	E	S	T	**V**	L	18
27	142	R	**V**	T	K	I	G	V	A	**A**	V	18
28	188	K	**L**	A	C	D	D	I	R	**V**	N	18
29	279	N	**I**	Y	L	L	V	P	P	**V**	L	18
30	291	I	**V**	Y	G	V	K	T	K	**E**	I	18

HLA-A3 decamers (SEQ ID NOS 2367-2432, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
31	294	G	**V**	K	T	K	E	I	R	**Q**	R	18
32	46	T	**I**	I	Y	I	V	R	T	**E**	H	17
33	102	Q	**I**	F	A	I	H	S	L	**S**	G	17
34	151	V	**V**	R	G	A	A	L	M	**A**	P	17
35	179	S	**Y**	C	L	H	Q	D	V	**M**	K	17
36	203	I	**V**	I	I	S	A	I	G	**L**	D	17
37	204	V	**I**	I	S	A	I	G	L	**D**	S	17
38	220	Y	**L**	L	I	L	K	T	V	**L**	G	17
39	221	L	**L**	I	L	K	T	V	L	**G**	L	17
40	227	V	**L**	G	L	T	R	E	A	**Q**	A	17
41	242	C	**V**	S	H	V	C	A	V	**F**	I	17
42	289	N	**P**	I	V	Y	G	V	K	**T**	K	17
43	38	L	**I**	A	V	L	G	N	L	**T**	I	16
44	85	A	**I**	F	W	F	N	S	T	**T**	I	16
45	147	G	**V**	A	A	V	V	R	G	**A**	A	16
46	198	V	**V**	Y	G	L	I	V	I	**I**	S	16
47	201	G	**L**	I	V	I	I	S	A	**I**	G	16
48	214	L	**L**	I	S	F	S	Y	L	**L**	I	16
49	226	T	**V**	L	G	L	T	R	E	**A**	Q	16
50	228	L	**G**	L	T	R	E	A	Q	**A**	K	16
51	229	G	**L**	T	R	E	A	Q	A	**K**	A	16
52	1	M	**V**	D	P	N	G	N	E	**S**	S	15
53	44	N	**L**	T	I	I	Y	I	V	**R**	T	15
54	47	I	**I**	Y	I	V	R	T	E	**H**	S	15
55	67	M	**L**	S	G	I	D	I	L	**I**	S	15
56	72	D	**I**	L	I	S	T	S	S	**M**	P	15
57	99	C	**L**	L	Q	I	F	A	I	**H**	S	15
58	105	A	**I**	H	S	L	S	G	M	**E**	S	15
59	145	K	**I**	G	V	A	A	V	V	**R**	G	15
60	175	I	**L**	S	H	S	Y	C	L	**H**	Q	15
61	191	C	**D**	D	I	R	V	N	V	**V**	Y	15
62	208	A	**I**	G	L	D	S	L	L	**I**	S	15
63	275	V	**I**	L	A	N	I	Y	L	**L**	V	15
64	281	Y	**L**	L	V	P	P	V	L	**N**	P	15
65	299	E	**I**	R	Q	R	I	L	R	**L**	F	15
66	306	R	**L**	F	H	V	A	T	H	**A**	S	15

HLA-B*0702 decamers (SEQ ID NOS 2433-2492, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
1	159	A	**P**	L	P	V	F	I	K	**Q**	L	23
2	59	E	**P**	M	Y	I	F	L	C	**M**	L	22
3	273	L	**P**	V	I	L	A	N	I	**Y**	L	20
4	3	D	**P**	N	G	N	E	S	S	**A**	T	19
5	130	H	**P**	L	R	H	A	T	V	**L**	T	19
6	140	L	**P**	R	V	T	K	I	G	**V**	A	19
7	161	L	**P**	V	F	I	K	Q	L	**P**	F	19
8	31	F	**P**	L	C	S	L	Y	L	**I**	A	18
9	271	S	**P**	L	P	V	I	L	A	**N**	I	18

HLA-B*0702 decamers (SEQ ID NOS 2433-2492, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
10	80	M	**P**	K	M	L	A	I	F	**W**	F	16
11	108	S	**L**	S	G	M	E	S	T	**V**	L	16
12	131	P	**L**	R	H	A	T	V	L	**T**	L	15
13	264	R	**F**	S	K	R	R	D	S	**P**	L	15
14	33	L	**C**	S	L	Y	L	I	A	**V**	L	14
15	109	L	**S**	G	M	E	S	T	V	**L**	L	14
16	152	V	**R**	G	A	A	L	M	A	**P**	L	14
17	205	I	**I**	S	A	I	G	L	D	**S**	L	14
18	215	L	**I**	S	F	S	Y	L	L	**I**	L	14
19	268	R	**R**	D	S	P	L	P	V	**I**	L	14
20	29	L	**A**	F	P	L	C	S	L	**Y**	L	13
21	148	V	**A**	A	V	V	R	G	A	**A**	L	13
22	156	A	**L**	M	A	P	L	P	V	**F**	I	13
23	193	D	**I**	R	V	N	V	V	Y	**G**	L	13
24	221	L	**L**	I	L	K	T	V	L	**G**	L	13
25	298	K	**E**	I	R	Q	R	I	L	**R**	L	13
26	7	N	**E**	S	S	A	T	Y	F	**I**	L	12
27	19	L	**P**	G	L	E	E	A	Q	**F**	W	12
28	24	E	**A**	Q	F	W	L	A	F	**P**	L	12
29	119	A	**M**	A	F	D	R	Y	V	**A**	I	12
30	129	C	**H**	P	L	R	H	A	T	**V**	L	12
31	206	I	**S**	A	I	G	L	D	S	**L**	L	12
32	219	S	**Y**	L	L	I	L	K	T	**V**	L	12
33	279	N	**I**	Y	L	L	V	P	P	**V**	L	12
34	285	P	**P**	V	L	N	P	I	V	**Y**	G	12
35	8	E	**S**	S	A	T	Y	F	I	**L**	I	11
36	13	Y	**F**	I	L	I	G	L	P	**G**	L	11
37	27	F	**W**	L	A	F	P	L	C	**S**	L	11
38	48	I	**Y**	I	V	R	T	E	H	**S**	L	11
39	56	S	**L**	H	E	P	M	Y	I	**F**	L	11
40	65	L	**C**	M	L	S	G	I	D	**I**	L	11
41	75	I	**S**	T	S	S	M	P	K	**M**	L	11
42	77	T	**S**	S	M	P	K	M	L	**A**	I	11
43	91	S	**T**	T	I	Q	F	D	A	**C**	L	11
44	123	D	**R**	Y	V	A	I	C	H	**P**	L	11
45	142	R	**V**	T	K	I	G	V	A	**A**	V	11
46	180	Y	**C**	L	H	Q	D	V	M	**K**	L	11
47	190	A	**C**	D	D	I	R	V	N	**V**	V	11
48	212	D	**S**	L	L	I	S	F	S	**Y**	L	11
49	234	A	**Q**	A	K	A	F	G	T	**C**	V	11
50	242	C	**V**	S	H	V	C	A	V	**F**	I	11
51	248	A	**V**	F	I	F	Y	V	P	**F**	I	11
52	250	F	**I**	F	Y	V	P	F	I	**G**	L	11
53	254	V	**P**	F	I	G	L	S	M	**V**	H	11
54	266	S	**K**	R	R	D	S	P	L	**P**	V	11
55	267	K	**R**	R	D	S	P	L	P	**V**	I	11
56	269	R	**D**	S	P	L	P	V	I	**L**	A	11
57	278	A	**N**	I	Y	L	L	V	P	**P**	V	11
58	284	V	**P**	P	V	L	N	P	I	**V**	Y	11
59	289	N	**P**	I	V	Y	G	V	K	**T**	K	11

HLA-B*0702 decamers(SEQ ID NOS 2433-2492, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	score
60	296	K	**T**	K	E	I	R	Q	R	I	L	11

Table XXVIII, beginning at page 205, line 1, has been amended as follows:

Table XXVIII:

HLA Class II Epitopes (sample 15-mer length)

(SEQ ID NOS 2493-2595, respectively in order of appearance)

HLA-DRB1*0101 15-mers

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	200	**Y**	G	L	**I**	V	**I**	I	S	**A**	I	G	L	D	S	L	36
2	68	**L**	S	G	**I**	D	**I**	L	I	**S**	T	S	S	M	P	K	34
3	62	**Y**	I	F	**L**	C	**M**	L	S	**G**	I	D	I	L	I	S	33
4	103	**I**	F	A	**I**	H	**S**	L	S	**G**	M	E	S	T	V	L	32
5	45	**L**	T	I	I	Y	**I**	V	R	**T**	E	H	S	L	H	E	31
6	193	**D**	I	R	**V**	N	**V**	V	Y	**G**	L	I	V	I	I	S	31
7	277	**L**	A	N	**I**	Y	**L**	L	V	**P**	P	V	L	N	P	I	31
8	97	**D**	A	C	**L**	L	**Q**	I	F	**A**	I	H	S	L	S	G	30
9	106	**I**	H	S	**L**	S	**G**	M	E	**S**	T	V	L	L	A	M	30
10	240	**G**	T	C	**V**	S	**H**	V	C	**A**	V	F	I	F	Y	V	30
11	10	**S**	A	T	**Y**	F	**I**	L	I	**G**	L	P	G	L	E	E	29
12	289	**N**	P	I	**V**	Y	**G**	V	K	**T**	K	E	I	R	Q	R	29
13	11	**A**	T	Y	**F**	I	**L**	I	G	**L**	P	G	L	E	E	A	28
14	250	**F**	I	F	**Y**	V	**P**	F	I	**G**	L	S	M	V	H	R	27
15	140	**L**	P	R	**V**	T	**K**	I	G	**V**	A	A	V	V	R	G	26
16	183	**H**	Q	D	**V**	M	**K**	L	A	**C**	D	D	I	R	V	N	26
17	217	**S**	F	S	**Y**	L	**L**	I	L	**K**	T	V	L	G	L	T	26
18	16	**L**	I	G	**L**	P	**G**	L	E	**E**	A	Q	F	W	L	A	25
19	24	**E**	A	Q	**F**	W	**L**	A	F	**P**	L	C	S	L	Y	L	25
20	36	**L**	Y	L	**I**	A	**V**	L	G	**N**	L	T	I	I	Y	I	25
21	70	**G**	I	D	**I**	L	**I**	S	T	**S**	S	M	P	K	M	L	25
22	111	**G**	M	E	**S**	T	**V**	L	L	**A**	M	A	F	D	R	Y	25
23	148	**V**	A	A	**V**	V	**R**	G	A	**A**	L	M	A	P	L	P	25
24	162	**P**	V	F	**I**	K	**Q**	L	P	**F**	C	R	S	N	I	L	25
25	197	**N**	V	V	**Y**	G	**L**	I	V	**I**	I	S	A	I	G	L	25
26	211	**L**	D	S	**L**	L	**I**	S	F	**S**	Y	L	L	I	L	K	25
27	218	**F**	S	Y	**L**	L	**I**	L	K	**T**	V	L	G	L	T	R	25
28	13	**Y**	F	I	**L**	I	**G**	L	P	**G**	L	E	E	A	Q	F	24
29	30	**A**	F	P	**L**	C	**S**	L	Y	**L**	I	A	V	L	G	N	24
30	39	**I**	A	V	**L**	G	**N**	L	T	**I**	I	Y	I	V	R	T	24
31	77	**T**	S	S	**M**	P	**K**	M	L	**A**	I	F	W	F	N	S	24
32	85	**A**	I	F	**W**	F	**N**	S	T	**T**	I	Q	F	D	A	C	24
33	137	**V**	L	T	**L**	P	**R**	V	T	**K**	I	G	V	A	A	V	24
34	151	**V**	V	R	**G**	A	**A**	L	M	**A**	P	L	P	V	F	I	24
35	161	**L**	P	V	**F**	I	**K**	Q	L	**P**	F	C	R	S	N	I	24
36	196	**V**	N	V	**V**	Y	**G**	L	I	**V**	I	I	S	A	I	G	24

HLA-DRB1*0101 15-mers

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
37	202	**L**	I	V	**I**	I	**S**	A	I	**G**	L	D	S	L	L	I	24
38	208	**A**	I	G	**L**	D	**S**	L	L	**I**	S	F	S	Y	L	L	24
39	248	**A**	V	F	**I**	F	**Y**	V	P	**F**	I	G	L	S	M	V	24
40	251	**I**	F	Y	**V**	P	**F**	I	G	**L**	S	M	V	H	R	F	24
41	83	**M**	L	A	**I**	F	**W**	F	N	**S**	T	T	I	Q	F	D	23
42	101	**L**	Q	I	**F**	A	**I**	H	S	**L**	S	G	M	E	S	T	23
43	165	**I**	K	Q	**L**	P	**F**	C	R	**S**	N	I	L	S	H	S	23
44	203	**I**	V	I	**I**	S	**A**	I	G	**L**	D	S	L	L	I	S	23
45	221	**L**	L	I	**L**	K	**T**	V	L	**G**	L	T	R	E	A	Q	23
46	278	**A**	N	I	**Y**	L	**L**	V	P	**P**	V	L	N	P	I	V	23
47	27	**F**	W	L	**A**	F	**P**	L	C	**S**	L	Y	L	I	A	V	22
48	35	**S**	L	Y	**L**	I	**A**	V	L	**G**	N	L	T	I	I	Y	22
49	61	**M**	Y	I	**F**	L	**C**	M	L	**S**	G	I	D	I	L	I	22
50	65	**L**	C	M	**L**	S	**G**	I	D	**I**	L	I	S	T	S	S	22
51	80	**M**	P	K	**M**	L	**A**	I	F	**W**	F	N	S	T	T	I	22
52	145	**K**	I	G	**V**	A	**A**	V	V	**R**	G	A	A	L	M	A	22
53	146	**I**	G	V	**A**	A	**V**	V	R	**G**	A	A	L	M	A	P	22
54	154	**G**	A	A	**L**	M	**A**	P	L	**P**	V	F	I	K	Q	L	22
55	205	**I**	I	S	**A**	I	**G**	L	D	**S**	L	L	I	S	F	S	22
56	243	**V**	S	H	**V**	C	**A**	V	F	**I**	F	Y	V	P	F	I	22
57	270	**D**	S	P	**L**	P	**V**	I	L	**A**	N	I	Y	L	L	V	22
58	274	**P**	V	I	**L**	A	**N**	I	Y	**L**	L	V	P	P	V	L	22
59	281	**Y**	L	L	**V**	P	**P**	V	L	**N**	P	I	V	Y	G	V	22
60	34	**C**	S	L	**Y**	L	**I**	A	V	**L**	G	N	L	T	I	I	21
61	69	**S**	G	I	**D**	I	**L**	I	S	**T**	S	S	M	P	K	M	21
62	152	**V**	R	G	**A**	A	**L**	M	A	**P**	L	P	V	F	I	K	21
63	299	**E**	I	R	**Q**	R	**I**	L	R	**L**	F	H	V	A	T	H	21
64	100	**L**	L	Q	**I**	F	**A**	I	H	**S**	L	S	G	M	E	S	20
65	135	**A**	T	V	**L**	T	**L**	P	R	**V**	T	K	I	G	V	A	20
66	141	**P**	R	V	**T**	K	**I**	G	V	**A**	A	V	V	R	G	A	20
67	191	**C**	D	D	**I**	R	**V**	N	V	**V**	Y	G	L	I	V	I	20
68	199	**V**	Y	G	**L**	I	**V**	I	I	**S**	A	I	G	L	D	S	20
69	262	**V**	H	R	**F**	S	**K**	R	R	**D**	S	P	L	P	V	I	20
70	271	**S**	P	L	**P**	V	**I**	L	A	**N**	I	Y	L	L	V	P	20
71	28	**W**	L	A	**F**	P	**L**	C	S	**L**	Y	L	I	A	V	L	19
72	58	**H**	E	P	**M**	Y	**I**	F	L	**C**	M	L	S	G	I	D	19
73	59	**E**	P	M	**Y**	I	**F**	L	C	**M**	L	S	G	I	D	I	19
74	60	**P**	M	Y	**I**	F	**L**	C	M	**L**	S	G	I	D	I	L	19
75	98	**A**	C	L	**L**	Q	**I**	F	A	**I**	H	S	L	S	G	M	19
76	215	**L**	I	S	**F**	S	**Y**	L	L	**I**	L	K	T	V	L	G	19
77	219	**S**	Y	L	**L**	I	**L**	K	T	**V**	L	G	L	T	R	E	19
78	228	**L**	G	L	**T**	R	**E**	A	Q	**A**	K	A	F	G	T	C	19
79	232	**R**	E	A	**Q**	A	**K**	A	F	**G**	T	C	V	S	H	V	19
80	246	**V**	C	A	**V**	F	**I**	F	Y	**V**	P	F	I	G	L	S	19
81	297	**T**	K	E	**I**	R	**Q**	R	I	**L**	R	L	F	H	V	A	19
82	3	**D**	P	N	**G**	N	**E**	S	S	**A**	T	Y	F	I	L	I	18
83	14	**F**	I	L	**I**	G	**L**	P	G	**L**	E	E	A	Q	F	W	18
84	25	**A**	Q	F	**W**	L	**A**	F	P	**L**	C	S	L	Y	L	I	18
85	42	**L**	G	N	**L**	T	**I**	I	Y	**I**	V	R	T	E	H	S	18
86	46	**T**	I	I	**Y**	I	**V**	R	T	**E**	H	S	L	H	E	P	18
87	78	**S**	S	M	**P**	K	**M**	L	A	**I**	F	W	F	N	S	T	18

HLA-DRB1*0101 15-mers

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
88	84	**L**	A	I	**F**	W	**F**	N	S	**T**	T	I	Q	F	D	A	18
89	89	**F**	N	S	**T**	T	**I**	Q	F	**D**	A	C	L	L	Q	I	18
90	93	**T**	I	Q	**F**	D	**A**	C	L	**L**	Q	I	F	A	I	H	18
91	115	**T**	V	L	**L**	A	**M**	A	F	**D**	R	Y	V	A	I	C	18
92	119	**A**	M	A	**F**	D	**R**	Y	V	**A**	I	C	H	P	L	R	18
93	127	**A**	I	C	**H**	P	**L**	R	H	**A**	T	V	L	T	L	P	18
94	129	**C**	H	P	**L**	R	**H**	A	T	**V**	L	T	L	P	R	V	18
95	147	**G**	V	A	**A**	V	**V**	R	G	**A**	A	L	M	A	P	L	18
96	149	**A**	A	V	**V**	R	**G**	A	A	**L**	M	A	P	L	P	V	18
97	216	**I**	S	F	**S**	Y	**L**	L	I	**L**	K	T	V	L	G	L	18
98	227	**V**	L	G	**L**	T	**R**	E	A	**Q**	A	K	A	F	G	T	18
99	249	**V**	F	I	**F**	Y	**V**	P	F	**I**	G	L	S	M	V	H	18
100	253	**Y**	V	P	**F**	I	**G**	L	S	**M**	V	H	R	F	S	K	18
101	284	**V**	P	P	**V**	L	**N**	P	I	**V**	Y	G	V	K	T	K	18
102	286	**P**	V	L	**N**	P	**I**	V	Y	**G**	V	K	T	K	E	I	18
103	303	**R**	I	L	**R**	L	**F**	H	V	**A**	T	H	A	S	E	P	18

HLA-DRB1*0301 (DR17) 15-mers
(SEQ ID NOS 2596-2671, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	16	**L**	I	G	**L**	P	**G**	L	E	**E**	A	Q	F	W	L	A	26
2	206	**I**	S	A	**I**	G	**L**	D	S	**L**	L	I	S	F	S	Y	23
3	91	**S**	T	T	**I**	Q	**F**	D	A	**C**	L	L	Q	I	F	A	22
4	117	**L**	L	A	**M**	A	**F**	D	R	**Y**	V	A	I	C	H	P	22
5	38	**L**	I	A	**V**	L	**G**	N	L	**T**	I	I	Y	I	V	R	21
6	179	**S**	Y	C	**L**	H	**Q**	D	V	**M**	K	L	A	C	D	D	21
7	211	**L**	D	S	**L**	L	**I**	S	F	**S**	Y	L	L	I	L	K	21
8	219	**S**	Y	L	**L**	I	**L**	K	T	**V**	L	G	L	T	R	E	21
9	272	**P**	L	P	**V**	I	**L**	A	N	**I**	Y	L	L	V	P	P	21
10	26	**Q**	F	W	**L**	A	**F**	P	L	**C**	S	L	Y	L	I	A	20
11	114	**S**	T	V	**L**	L	**A**	M	A	**F**	D	R	Y	V	A	I	20
12	129	**C**	H	P	**L**	R	**H**	A	T	**V**	L	T	L	P	R	V	20
13	134	**H**	A	T	**V**	L	**T**	L	P	**R**	V	T	K	I	G	V	20
14	186	**V**	M	K	**L**	A	**C**	D	D	**I**	R	V	N	V	V	Y	20
15	200	**Y**	G	L	**I**	V	**I**	I	S	**A**	I	G	L	D	S	L	20
16	270	**D**	S	P	**L**	P	**V**	I	L	**A**	N	I	Y	L	L	V	20
17	297	**T**	K	E	**I**	R	**Q**	R	I	**L**	R	L	F	H	V	A	20
18	11	**A**	T	Y	**F**	I	**L**	I	G	**L**	P	G	L	E	E	A	19
19	54	**E**	H	S	**L**	H	**E**	P	M	**Y**	I	F	L	C	M	L	19
20	106	**I**	H	S	**L**	S	**G**	M	E	**S**	T	V	L	L	A	M	19
21	165	**I**	K	Q	**L**	P	**F**	C	R	**S**	N	I	L	S	H	S	19
22	191	**C**	D	D	**I**	R	**V**	N	V	**V**	Y	G	L	I	V	I	19
23	203	**I**	V	I	**I**	S	**A**	I	G	**L**	D	S	L	L	I	S	19
24	213	**S**	L	L	**I**	S	**F**	S	Y	**L**	L	I	L	K	T	V	19
25	224	**L**	K	T	**V**	L	**G**	L	T	**R**	E	A	Q	A	K	A	19
26	227	**V**	L	G	**L**	T	**R**	E	A	**Q**	A	K	A	F	G	T	19
27	248	**A**	V	F	**I**	F	**Y**	V	P	**F**	I	G	L	S	M	V	19
28	254	**V**	P	F	**I**	G	**L**	S	M	**V**	H	R	F	S	K	R	19
29	277	**L**	A	N	**I**	Y	**L**	L	V	**P**	P	V	L	N	P	I	19

HLA-DRB1*0301 (DR17) 15-mers
(SEQ ID NOS 2596-2671, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
30	36	**L**	Y	L	**I**	A	**V**	L	G	**N**	L	T	I	I	Y	I	18
31	93	**T**	I	Q	**F**	D	**A**	C	L	**L**	Q	I	F	A	I	H	18
32	98	**A**	C	L	**L**	Q	**I**	F	A	**I**	H	S	L	S	G	M	18
33	125	**Y**	V	A	**I**	C	**H**	P	L	**R**	H	A	T	V	L	T	18
34	158	**M**	A	P	**L**	P	**V**	F	I	**K**	Q	L	P	F	C	R	18
35	187	**M**	K	L	**A**	C	**D**	D	I	**R**	V	N	V	V	Y	G	18
36	217	**S**	F	S	**Y**	L	**L**	I	L	**K**	T	V	L	G	L	T	18
37	225	**K**	T	V	**L**	G	**L**	T	R	**E**	A	Q	A	K	A	F	18
38	281	**Y**	L	L	**V**	P	**P**	V	L	**N**	P	I	V	Y	G	V	18
39	288	**L**	N	P	**I**	V	**Y**	G	V	**K**	T	K	E	I	R	Q	18
40	18	**G**	L	P	**G**	L	**E**	E	A	**Q**	F	W	L	A	F	P	17
41	44	**N**	L	T	**I**	I	**Y**	I	V	**R**	T	E	H	S	L	H	17
42	145	**K**	I	G	**V**	A	**A**	V	V	**R**	G	A	A	L	M	A	17
43	159	**A**	P	L	**P**	V	**F**	I	K	**Q**	L	P	F	C	R	S	17
44	256	**F**	I	G	**L**	S	**M**	V	H	**R**	F	S	K	R	R	D	17
45	259	**L**	S	M	**V**	H	**R**	F	S	**K**	R	R	D	S	P	L	17
46	137	**V**	L	T	**L**	P	**R**	V	T	**K**	I	G	V	A	A	V	16
47	262	**V**	H	R	**F**	S	**K**	R	R	**D**	S	P	L	P	V	I	16
48	294	**G**	V	K	**T**	K	**E**	I	R	**Q**	R	I	L	R	L	F	16
49	46	**T**	I	I	**Y**	I	**V**	R	T	**E**	H	S	L	H	E	P	15
50	51	**V**	R	T	**E**	H	**S**	L	H	**E**	P	M	Y	I	F	L	15
51	172	**R**	S	N	**I**	L	**S**	H	S	**Y**	C	L	H	Q	D	V	15
52	189	**L**	A	C	**D**	D	**I**	R	V	**N**	V	V	Y	G	L	I	15
53	212	**D**	S	L	**L**	I	**S**	F	S	**Y**	L	L	I	L	K	T	15
54	218	**F**	S	Y	**L**	L	**I**	L	K	**T**	V	L	G	L	T	R	15
55	271	**S**	P	L	**P**	V	**I**	L	A	**N**	I	Y	L	L	V	P	15
56	279	**N**	I	Y	**L**	L	**V**	P	P	**V**	L	N	P	I	V	Y	15
57	12	**T**	Y	F	**I**	L	**I**	G	L	**P**	G	L	E	E	A	Q	14
58	35	**S**	L	Y	**L**	I	**A**	V	L	**G**	N	L	T	I	I	Y	14
59	64	**F**	L	C	**M**	L	**S**	G	I	**D**	I	L	I	S	T	S	14
60	140	**L**	P	R	**V**	T	**K**	I	G	**V**	A	A	V	V	R	G	14
61	273	**L**	P	V	**I**	L	**A**	N	I	**Y**	L	L	V	P	P	V	14
62	301	**R**	Q	R	**I**	L	**R**	L	F	**H**	V	A	T	H	A	S	14
63	13	**Y**	F	I	**L**	I	**G**	L	P	**G**	L	E	E	A	Q	F	13
64	47	**I**	I	Y	**I**	V	**R**	T	E	**H**	S	L	H	E	P	M	13
65	71	**I**	D	I	**L**	I	**S**	T	S	**S**	M	P	K	M	L	A	13
66	80	**M**	P	K	**M**	L	**A**	I	F	**W**	F	N	S	T	T	I	13
67	109	**L**	S	G	**M**	E	**S**	T	V	**L**	L	A	M	A	F	D	13
68	113	**E**	S	T	**V**	L	**L**	A	M	**A**	F	D	R	Y	V	A	13
69	135	**A**	T	V	**L**	T	**L**	P	R	**V**	T	K	I	G	V	A	13
70	195	**R**	V	N	**V**	V	**Y**	G	L	**I**	V	I	I	S	A	I	13
71	202	**L**	I	V	**I**	I	**S**	A	I	**G**	L	D	S	L	L	I	13
72	220	**Y**	L	L	**I**	L	**K**	T	V	**L**	G	L	T	R	E	A	13
73	221	**L**	L	I	**L**	K	**T**	V	L	**G**	L	T	R	E	A	Q	13
74	264	**R**	F	S	**K**	R	**R**	D	S	**P**	L	P	V	I	L	A	13
75	280	**I**	Y	L	**L**	V	**P**	P	V	**L**	N	P	I	V	Y	G	13
76	302	**Q**	R	I	**L**	R	**L**	F	H	**V**	A	T	H	A	S	E	13

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	36	**L**	Y	L	**I**	A	**V**	**L**	G	**N**	L	T	I	I	Y	I	26
2	45	**L**	T	I	**I**	Y	**I**	**V**	R	**T**	E	H	S	L	H	E	26
3	68	**L**	S	G	**I**	D	**I**	**L**	I	**S**	T	S	S	M	P	K	26
4	83	**M**	L	A	**I**	F	**W**	**F**	N	**S**	T	T	I	Q	F	D	26
5	134	**H**	A	T	**V**	L	**T**	**L**	P	**R**	V	T	K	I	G	V	26
6	145	**K**	I	G	**V**	A	**A**	**V**	V	**R**	G	A	A	L	M	A	26
7	224	**L**	K	T	**V**	L	**G**	**L**	T	**R**	E	A	Q	A	K	A	26
8	227	**V**	L	G	**L**	T	**R**	**E**	A	**Q**	A	K	A	F	G	T	26
9	256	**F**	I	G	**L**	S	**M**	**V**	H	**R**	F	S	K	R	R	D	26
10	281	**Y**	L	L	**V**	P	**P**	**V**	L	**N**	P	I	V	Y	G	V	26
11	289	**N**	P	I	**V**	Y	**G**	**V**	K	**T**	K	E	I	R	Q	R	26
12	301	**R**	Q	R	**I**	L	**R**	**L**	F	**H**	V	A	T	H	A	S	26
13	11	**A**	T	Y	**F**	I	**L**	**I**	G	**L**	P	G	L	E	E	A	22
14	24	**E**	A	Q	**F**	W	**L**	**A**	F	**P**	L	C	S	L	Y	L	22
15	25	**A**	Q	F	**W**	L	**A**	**F**	P	**L**	C	S	L	Y	L	I	22
16	34	**C**	S	L	**Y**	L	**I**	**A**	V	**L**	G	N	L	**T**	I	I	22
17	84	**L**	A	I	**F**	W	**F**	**N**	S	**T**	T	I	Q	F	D	A	22
18	122	**F**	D	R	**Y**	V	**A**	**I**	C	**H**	P	L	R	H	A	T	22
19	197	**N**	V	V	**Y**	G	**L**	**I**	V	**I**	I	S	A	I	G	L	22
20	215	**L**	I	S	**F**	S	**Y**	**L**	L	**I**	L	K	T	V	L	G	22
21	217	**S**	F	S	**Y**	L	**L**	**I**	L	**K**	T	V	L	G	L	T	22
22	250	**F**	I	F	**Y**	V	**P**	**F**	I	**G**	L	S	M	V	H	R	22
23	278	**A**	N	I	**Y**	L	**L**	**V**	P	**P**	V	L	N	P	I	V	22
24	19	**L**	P	G	**L**	E	**E**	**A**	Q	**F**	W	L	A	F	P	L	20
25	30	**A**	F	P	**L**	C	**S**	**L**	Y	**L**	I	A	V	L	G	N	20
26	33	**L**	C	S	**L**	Y	**L**	**I**	A	**V**	L	G	N	L	T	I	20
27	35	**S**	L	Y	**L**	I	**A**	**V**	L	**G**	N	L	T	I	I	Y	20
28	39	**I**	A	V	**L**	G	**N**	**L**	T	**I**	I	Y	I	V	R	T	20
29	42	**L**	G	N	**L**	T	**I**	**I**	Y	**I**	V	R	T	E	H	S	20
30	44	**N**	L	T	**I**	I	**Y**	**I**	V	**R**	T	E	H	S	L	H	20
31	48	**I**	Y	I	**V**	R	**T**	**E**	H	**S**	L	H	E	P	M	Y	20
32	58	**H**	E	P	**M**	Y	**I**	**F**	L	**C**	M	L	S	G	I	D	20
33	62	**Y**	I	F	**L**	C	**M**	**L**	S	**G**	I	D	I	L	I	S	20
34	65	**L**	C	M	**L**	S	**G**	**I**	D	**I**	L	I	S	T	S	S	20
35	71	**I**	D	I	**L**	I	**S**	**T**	S	**S**	M	P	K	M	L	A	20
36	80	**M**	P	K	**M**	L	**A**	**I**	F	**W**	F	N	S	T	T	I	20
37	81	**P**	K	M	**L**	A	**I**	**F**	W	**F**	N	S	T	T	I	Q	20
38	91	**S**	T	T	**I**	Q	**F**	**D**	A	**C**	L	L	Q	I	F	A	20
39	97	**D**	A	C	**L**	L	**Q**	**I**	F	**A**	I	H	S	L	S	G	20
40	98	**A**	C	L	**L**	Q	**I**	**F**	A	**I**	H	S	L	S	G	M	20
41	100	**L**	L	Q	**I**	F	**A**	**I**	H	**S**	L	S	G	M	E	S	20
42	103	**I**	F	A	**I**	H	**S**	**L**	S	**G**	M	E	S	T	V	L	20
43	106	**I**	H	S	**L**	S	**G**	**M**	E	**S**	T	V	L	L	A	M	20
44	115	**T**	V	L	**L**	A	**M**	**A**	F	**D**	R	Y	V	A	I	C	20
45	117	**L**	L	A	**M**	A	**F**	**D**	R	**Y**	V	A	I	C	H	P	20
46	125	**Y**	V	A	**I**	C	**H**	**P**	L	**R**	H	A	T	V	L	T	20
47	129	**C**	H	P	**L**	R	**H**	**A**	T	**V**	L	T	L	P	R	V	20
48	137	**V**	L	T	**L**	P	**R**	**V**	T	**K**	I	G	V	A	A	V	20
49	140	**L**	P	R	**V**	T	**K**	**I**	G	**V**	A	A	V	V	R	G	20

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
50	155	A	A	L	M	A	P	L	P	V	F	I	K	Q	L	P	20
51	162	P	V	F	I	K	Q	L	P	F	C	R	S	N	I	L	20
52	165	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	S	20
53	179	S	Y	C	L	H	Q	D	V	M	K	L	A	C	D	D	20
54	183	H	Q	D	V	M	K	L	A	C	D	D	I	R	V	N	20
55	186	V	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	20
56	193	D	I	R	V	N	V	V	Y	G	L	I	V	I	I	S	20
57	196	V	N	V	V	Y	G	L	I	V	I	I	S	A	I	G	20
58	199	V	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	20
59	200	Y	G	L	I	V	I	I	S	A	I	G	L	D	S	L	20
60	202	L	I	V	I	I	S	A	I	G	L	D	S	L	L	I	20
61	203	I	V	I	I	S	A	I	G	L	D	S	L	L	I	S	20
62	206	I	S	A	I	G	L	D	S	L	L	I	S	F	S	Y	20
63	208	A	I	G	L	D	S	L	L	I	S	F	S	Y	L	L	20
64	211	L	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	20
65	212	D	S	L	L	I	S	F	S	Y	L	L	I	L	K	T	20
66	218	F	S	Y	L	L	I	L	K	T	V	L	G	L	T	R	20
67	240	G	T	C	V	S	H	V	C	A	V	F	I	F	Y	V	20
68	243	V	S	H	V	C	A	V	F	I	F	Y	V	P	F	I	20
69	246	V	C	A	V	F	I	F	Y	V	P	F	I	G	L	S	20
70	248	A	V	F	I	F	Y	V	P	F	I	G	L	S	M	V	20
71	251	I	F	Y	V	P	F	I	G	L	S	M	V	H	R	F	20
72	272	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	P	20
73	277	L	A	N	I	Y	L	L	V	P	P	V	L	N	P	I	20
74	285	P	P	V	L	N	P	I	V	Y	G	V	K	T	K	E	20
75	18	G	L	P	G	L	E	E	A	Q	F	W	L	A	F	P	18
76	27	F	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	18
77	69	S	G	I	D	I	L	I	S	T	S	S	M	P	K	M	18
78	94	I	Q	F	D	A	C	L	L	Q	I	F	A	I	H	S	18
79	99	C	L	L	Q	I	F	A	I	H	S	L	S	G	M	E	18
80	107	H	S	L	S	G	M	E	S	T	V	L	L	A	M	A	18
81	116	V	L	L	A	M	A	F	D	R	Y	V	A	I	C	H	18
82	126	V	A	I	C	H	P	L	R	H	A	T	V	L	T	L	18
83	164	F	I	K	Q	L	P	F	C	R	S	N	I	L	S	H	18
84	176	L	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	18
85	187	M	K	L	A	C	D	D	I	R	V	N	V	V	Y	G	18
86	205	I	I	S	A	I	G	L	D	S	L	L	I	S	F	S	18
87	233	E	A	Q	A	K	A	F	G	T	C	V	S	H	V	C	18
88	237	K	A	F	G	T	C	V	S	H	V	C	A	V	F	I	18
89	271	S	P	L	P	V	I	L	A	N	I	Y	L	L	V	P	18
90	293	Y	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	18
91	294	G	V	K	T	K	E	I	R	Q	R	I	L	R	L	F	18
92	10	S	A	T	Y	F	I	L	I	G	L	P	G	L	E	E	16
93	28	W	L	A	F	P	L	C	S	L	Y	L	I	A	V	L	16
94	59	E	P	M	Y	I	F	L	C	M	L	S	G	I	D	I	16
95	61	M	Y	I	F	L	C	M	L	S	G	I	D	I	L	I	16
96	85	A	I	F	W	F	N	S	T	T	I	Q	F	D	A	C	16
97	101	L	Q	I	F	A	I	H	S	L	S	G	M	E	S	T	16
98	177	S	H	S	Y	C	L	H	Q	D	V	M	K	L	A	C	16

HLA-DRB1*0401 (DR4Dw4) 15-mers
(SEQ ID NOS 2672-2805, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
99	236	**A**	K	A	**F**	G	**T**	**C**	V	**S**	H	V	C	A	V	F	16
100	249	**V**	F	I	**F**	Y	**V**	**P**	F	**I**	G	L	S	M	V	H	16
101	253	**Y**	V	P	**F**	I	**G**	**L**	S	**M**	V	H	R	F	S	K	16
102	13	**Y**	F	I	**L**	I	**G**	**L**	P	**G**	L	E	E	A	Q	F	14
103	14	**F**	I	L	**I**	G	**L**	**P**	G	**L**	E	E	A	Q	F	W	14
104	16	**L**	I	G	**L**	P	**G**	**L**	E	**E**	A	Q	F	W	L	A	14
105	38	**L**	I	A	**V**	L	**G**	**N**	L	**T**	I	I	Y	I	V	R	14
106	47	**I**	I	Y	**I**	V	**R**	**T**	E	**H**	S	L	H	E	P	M	14
107	54	**E**	H	S	**L**	H	**E**	**P**	M	**Y**	I	F	L	C	M	L	14
108	60	**P**	M	Y	**I**	F	**L**	**C**	M	**L**	S	G	I	D	I	L	14
109	64	**F**	L	C	**M**	L	**S**	**G**	I	**D**	I	L	I	S	T	S	14
110	70	**G**	I	D	**I**	L	**I**	**S**	T	**S**	S	M	P	K	M	L	14
111	72	**D**	I	L	**I**	S	**T**	**S**	S	**M**	P	K	M	L	A	I	14
112	109	**L**	S	G	**M**	E	**S**	**T**	V	**L**	L	A	M	A	F	D	14
113	113	**E**	S	T	**V**	L	**L**	**A**	M	**A**	F	D	R	Y	V	A	14
114	135	**A**	T	V	**L**	T	**L**	**P**	R	**V**	T	K	I	G	V	A	14
115	143	**V**	T	K	**I**	G	**V**	**A**	A	**V**	V	R	G	A	A	L	14
116	148	**V**	A	A	**V**	V	**R**	**G**	A	**A**	L	M	A	P	L	P	14
117	149	**A**	A	V	**V**	R	**G**	**A**	A	**L**	M	A	P	L	P	V	14
118	154	**G**	A	A	**L**	M	**A**	**P**	L	**P**	V	F	I	K	Q	L	14
119	158	**M**	A	P	**L**	P	**V**	**F**	I	**K**	Q	L	P	F	C	R	14
120	173	**S**	N	I	**L**	S	**H**	**S**	Y	**C**	L	H	Q	D	V	M	14
121	184	**Q**	D	V	**M**	K	**L**	**A**	C	**D**	D	I	R	V	N	V	14
122	191	**C**	D	D	**I**	R	**V**	**N**	V	**V**	Y	G	L	I	V	I	14
123	195	**R**	V	N	**V**	V	**Y**	**G**	L	**I**	V	I	I	S	A	I	14
124	213	**S**	L	L	**I**	S	**F**	**S**	Y	**L**	L	I	L	K	T	V	14
125	220	**Y**	L	L	**I**	L	**K**	**T**	V	**L**	G	L	T	R	E	A	14
126	221	**L**	L	I	**L**	K	**T**	**V**	L	**G**	L	T	R	E	A	Q	14
127	225	**K**	T	V	**L**	G	**L**	**T**	R	**E**	A	Q	A	K	A	F	14
128	259	**L**	S	M	**V**	H	**R**	**F**	S	**K**	R	R	D	S	P	L	14
129	270	**D**	S	P	**L**	P	**V**	**I**	L	**A**	N	I	Y	L	L	V	14
130	273	**L**	P	V	**I**	L	**A**	**N**	I	**Y**	L	L	V	P	P	V	14
131	274	**P**	V	I	**L**	A	**N**	**I**	Y	**L**	L	V	P	P	V	L	14
132	280	**I**	Y	L	**L**	V	**P**	**P**	V	**L**	N	P	I	V	Y	G	14
133	284	**V**	P	P	**V**	L	**N**	**P**	I	**V**	Y	G	V	K	T	K	14
134	302	**Q**	R	I	**L**	R	**L**	**F**	H	**V**	A	T	H	A	S	E	14

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
1	145	**K**	I	G	**V**	A	**A**	V	V	**R**	G	A	A	L	M	A	28
2	122	**F**	D	R	**Y**	V	**A**	I	C	**H**	P	L	R	H	A	T	25
3	217	**S**	F	S	**Y**	L	**L**	I	L	**K**	T	V	L	G	L	T	25
4	197	**N**	V	V	**Y**	G	**L**	I	V	**I**	I	S	A	I	G	L	24
5	10	**S**	A	T	**Y**	F	**I**	L	I	**G**	L	P	G	L	E	E	23
6	255	**P**	F	I	**G**	L	**S**	M	V	**H**	R	F	S	K	R	R	23
7	44	**N**	L	T	**I**	I	**Y**	I	V	**R**	T	E	H	S	L	H	22

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
8	59	**E**	P	M	**Y**	I	**F**	L	C	**M**	L	S	G	I	D	I	22
9	158	**M**	A	P	**L**	P	**V**	F	I	**K**	Q	L	P	F	C	R	22
10	237	**K**	A	F	**G**	T	**C**	V	S	**H**	V	C	A	V	F	I	22
11	74	**L**	I	S	**T**	S	**S**	M	P	**K**	M	L	A	I	F	W	21
12	134	**H**	A	T	**V**	L	**T**	L	P	**R**	V	T	K	I	G	V	20
13	137	**V**	L	T	**L**	P	**R**	V	T	**K**	I	G	V	A	A	V	20
14	162	**P**	V	F	**I**	K	**Q**	L	P	**F**	C	R	S	N	I	L	20
15	199	**V**	Y	G	**L**	I	**V**	I	I	**S**	A	I	G	L	D	S	20
16	224	**L**	K	T	**V**	L	**G**	L	T	**R**	E	A	Q	A	K	A	20
17	256	**F**	I	G	**L**	S	**M**	V	H	**R**	F	S	K	R	R	D	20
18	290	**P**	I	V	**Y**	G	**V**	K	T	**K**	E	I	R	Q	R	I	20
19	301	**R**	Q	R	**I**	L	**R**	L	F	**H**	V	A	T	H	A	S	20
20	65	**L**	C	M	**L**	S	**G**	I	D	**I**	L	I	S	T	S	S	19
21	100	**L**	L	Q	**I**	F	**A**	I	H	**S**	L	S	G	M	E	S	19
22	196	**V**	N	V	**V**	Y	**G**	L	I	**V**	I	I	S	A	I	G	19
23	218	**F**	S	Y	**L**	L	**I**	L	K	**T**	V	L	G	L	T	R	19
24	247	**C**	A	V	**F**	I	**F**	Y	V	**P**	F	I	G	L	S	M	19
25	274	**P**	V	I	**L**	A	**N**	I	Y	**L**	L	V	P	P	V	L	19
26	45	**L**	T	I	**I**	Y	**I**	V	R	**T**	E	H	S	L	H	E	18
27	68	**L**	S	G	**I**	D	**I**	L	I	**S**	T	S	S	M	P	K	18
28	80	**M**	P	K	**M**	L	**A**	I	F	**W**	F	N	S	T	T	I	18
29	97	**D**	A	C	**L**	L	**Q**	I	F	**A**	I	H	S	L	S	G	18
30	103	**I**	F	A	**I**	H	**S**	L	S	**G**	M	E	S	T	V	L	18
31	208	**A**	I	G	**L**	D	**S**	L	L	**I**	S	F	S	Y	L	L	18
32	249	**V**	F	I	**F**	Y	**V**	P	F	**I**	G	L	S	M	V	H	18
33	61	**M**	Y	I	**F**	L	**C**	M	L	**S**	G	I	D	I	L	I	17
34	215	**L**	I	S	**F**	S	**Y**	L	L	**I**	L	K	T	V	L	G	17
35	259	**L**	S	M	**V**	H	**R**	F	S	**K**	R	R	D	S	P	L	17
36	278	**A**	N	I	**Y**	L	**L**	V	P	**P**	V	L	N	P	I	V	17
37	288	**L**	N	P	**I**	V	**Y**	G	V	**K**	T	K	E	I	R	Q	17
38	11	**A**	T	Y	**F**	I	**L**	I	G	**L**	P	G	L	E	E	A	16
39	24	**E**	A	Q	**F**	W	**L**	A	F	**P**	L	C	S	L	Y	L	16
40	42	**L**	G	N	**L**	T	**I**	I	Y	**I**	V	R	T	E	H	S	16
41	253	**Y**	V	P	**F**	I	**G**	L	S	**M**	V	H	R	F	S	K	16
42	47	**I**	I	Y	**I**	V	**R**	T	E	**H**	S	L	H	E	P	M	15
43	99	**C**	L	L	**Q**	I	**F**	A	I	**H**	S	L	S	G	M	E	15
44	116	**V**	L	L	**A**	M	**A**	F	D	**R**	Y	V	A	I	C	H	15
45	143	**V**	T	K	**I**	G	**V**	A	A	**V**	V	R	G	A	A	L	15
46	179	**S**	Y	C	**L**	H	**Q**	D	V	**M**	K	L	A	C	D	D	15
47	227	**V**	L	G	**L**	T	**R**	E	A	**Q**	A	K	A	F	G	T	15
48	260	**S**	M	V	**H**	R	**F**	S	K	**R**	R	D	S	P	L	P	15
49	261	**M**	V	H	**R**	F	**S**	K	R	**R**	D	S	P	L	P	V	15
50	277	**L**	A	N	**I**	Y	**L**	L	V	**P**	P	V	L	N	P	I	15
51	285	**P**	P	V	**L**	N	**P**	I	V	**Y**	G	V	K	T	K	E	15
52	114	**S**	T	V	**L**	L	**A**	M	A	**F**	D	R	Y	V	A	I	14
53	125	**Y**	V	A	**I**	C	**H**	P	L	**R**	H	A	T	V	L	T	14
54	126	**V**	A	I	**C**	H	**P**	L	R	**H**	A	T	V	**L**	T	L	14
55	140	**L**	P	R	**V**	T	**K**	I	G	**V**	A	A	V	V	R	G	14
56	170	**F**	C	R	**S**	N	**I**	L	S	**H**	S	Y	C	L	H	Q	14

HLA-DRB1*1101 15-mers
(SEQ ID NOS 2806-2866, respectively in order of appearance)

	Pos	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	score
57	180	**Y**	C	L	**H**	Q	**D**	V	M	**K**	L	A	C	D	D	I	14
58	193	**D**	I	R	**V**	N	**V**	V	Y	**G**	L	I	V	I	I	S	14
59	229	**G**	L	T	**R**	E	**A**	Q	A	**K**	A	F	G	T	C	V	14
60	270	**D**	S	P	**L**	P	**V**	I	L	**A**	N	I	Y	L	L	V	14
61	298	**K**	E	I	**R**	Q	**R**	I	L	**R**	L	F	H	V	A	T	14

Table XXIX, beginning at page 213, line 1, has been amended as follows:

Table XXIX. Nucleotide sequence in the 5' region close to 101P3A11 gene (SEQ ID NO: 2867).

```
   1 TGCGCTCCAC CAAGCCTGGC TAACTTTTGC ATTTTTAATA GAGGCAGGGT TTCACCATGT
  61 TGGCCTGGCT GGTCTCGAAC CCCTGACCTT GCGATCTGCC CACCTCGGCC TCCCAAAGTG
 121 CTGGGATTAC AGGCGTGAGC CACTGTACCT GGCGGGGCTT ATTGTTTTTT AAAAAGATTT
 181 CCAAAACCTT GCCCTGGCAA TTCTGATTTT CTGGGCCTGG AGCAGGACCT GGAGGGATGG
 241 TGTTGTCAAT TACTTTAGAT GTTTCTATCA GGAAAGTTTG AGAAATGGTA TTCAGGCCTA
 301 AACACAAACC TCTCTTGAAA TCTCATCCCA GACTGAGCCC CTGCTCCCTA TCTTAAATTA
 361 GATTATAGTA GGTCTTAAAG TCAGCTGTAG ACTGAGCCTC TAAATCTGAA CCCAGACCCA
 421 CCCTAACCCC AGGATACATC AGAAGAGCTG GTCAATGTGG ACCATTCTGA GCAATCCTGC
 481 AAGTCTACTC TGATGGGAAA AGGCTAAGAG CAGTGCCCTG GGCAGCAACA TCAGCTCTGA
 541 AGATGCAGGA CTGTGTTACA TGTTTTATGA GTGGGTCTTC ACACACTGAG ATTCATGGGA
 601 CAGTAATAGA ATCTGCTTGT GCAGCACTGG GGCCTTGGAG GGTCAGGGTA AGGCTCAAGA
 661 TGTCCAGGAA GTTGTATATA AGGAGAATCA GAGCAGAGAG AGACTAGGGT TCAGAATTAC
 721 CAGGATGACT TAGTCCTGTT TGTTACTGTC ACCACTCCAA TGCCTTTTCC TCATTAGTCC
 781 TTTCTCTCCT CTGAGCCACA ACTAAATGAT GTTTCTACTT TTCCCTTTCT ACTTTCCTAG
 841 ACCCTGGATT TTGTATGCAG AAGCCCCAGC TCTTGGTCCC TATCATAGCC ACTTCAAATG
 901 GAAATCTGGT CCACGCAGCA TACTTCCTTT TGGTGGGTAT CCCTGGCCTG GGGCCTACCA
 961 TACACTTTTG GCTGGCTTTC CCACTGTGTT TTATGTATGC CTTGGCCACC CTGGGTAACC
1021 TGACCATTGT CCTCATCATT CGTGTGGAGA GGCGACTGCA TGAGCCCATG TACCTCTTCC
1081 TGGCCATGCT TTCCACTATT GACCTAGTCC TCTCCTCTAT CACCATGCCC AAGATGGCCA
1141 GTCTTTTCCT GATGGGCATC CAGGAGATCG AGTTCAACAT TTGCCTGGCC CAGATGTTCC
1201 TTATCCATGC TCTGTCAGCC GTGGAGTCAG CTGTCCTGCT GGCCATGGCT TTTGACCGCT
1261 TTGTGGCCAT TTGCCACCCA TTGCGCCATG CTTCTGTGCT GACAGGGTGT ACTGTGGCCA
1321 AGATTGGACT ATCTGCCCTG ACCAGGGGGT TTGTATTCTT CTTCCCACTG CCCTTCATCC
1381 TCAAGTGGTT GTCCTACTGC CAAACACATA CTGTCACACA CTCCTTCTGT CTGCACCAAG
1441 ATATTATGAA GCTGTCCTGT ACTGACACCA GGGTCAATGT GGTTTATGGA CTCTTCATCA
1501 TCCTCTCAGT CATGGGTGTG GACTCTCTCT TCATTGGCTT CTCATATATC CTCATCCTGT
1561 GGGCTGTTTT GGAGCTGTCC TCTCGGAGGG CAGCACTCAA GGCTTTCAAC ACCTGCATCT
1621 CCCACCTCTG TGCTGTTCTG GTCTTCTATG TACCCCTCAT TGGGCTCTCG GTGGTGCATA
1681 GGCTGGGTGG TCCCACCTCC CTCCTCCATG TGGTTATGGC TAATACCTAC TTGCTGCTAC
1741 CACCTGTAGT CAACCCCCTT GTCTATGGAG CCAAGACCAA AGAGATCTGT TCAAGGGTCC
1801 TCTGTATGTT CTCACAAGGT GGCAAGTGAG ACACCTTAGT GTCTCGCTTC TACTACTACT
1861 ACAGAAGATG GGAATATTAG GATCCTATTG AATGCCTTGG TGATTAAAGT ATCAAACCTA
1921 TTGTGCTGTC TTCTTCCAGC AATTTAAGTA GATCATGTAT TCTGTCTCCA GGAATGTGTC
1981 AGTACTGAAC TTATGACCCT GTCTGGACAT CCTGGAGAAT GACTGCACTA GTCCCTCTGC
2041 TATGGTGGTC TTGCCTTCTC CTTCTCTCTC AGCTAGAAAA TACATCTAGT TTTGACATGG
2101 GGAGGCTGTA AAGATCACAC CTCATGGTTC ATTCCAGTTT TGAAGTATGA TTTTAATGTT
```

2161 CTTGCCCCCA TGTGCCCATG TTGGTGAATT TGCATGGACT ATAAACGTTA TTGCAAATAC
2221 CCTAAAGTGG TTACCCAGCC ATAATCAGGG GTTAATGAAG GTATTTGGGG AATAGTAACT
2281 GGAGAGACAG CAACAAGACA AGAGGCAGCT CACATGCAAT GTTGAAGTTT CTGTATGCAA
2341 GAGGGTGTGT TGGCAGATTT GTGAAATCTG CCCATTTGCA TCTGTATGGC TCTATATGAC
2401 TATTTGTCCA TAAGGGTGCC ATGTATTCTG GTTGTGGGTG TGAATGTGTG GGTGTGTTTA
2461 TGTGGACACT TGCTTTTCAG TGTGCGTATA TGTGAGAGAG AGGGTGCACA CATGGAATAC
2521 GTACTGGTTG TGTCCTGGTG AGTGTGGTAG CTATGTCCTG GCACATGTAT GTTTCATGAG
2581 ACGTGTCTCT GATTGCGCAT TTGTATTTCT GTGGTATCTG TTAGTTGGTA TATGATATGT
2641 GTCTACGTGA GAATGCTGGT GTCTGTATCT GCATGGTGGG CAGTACCTTT ATGTGTATCT
2701 GGTAAGAATG CTGCCTCTAC CTTTTCTTCC TATTTGTACT ATGTGAATGT GGTGCATGAA
2761 TGTGTGGAAT GTGTGGAATG TGTAGTATTG GGATGCCTGT ATCTTTCAGC GTGTTTGGGT
2821 GTATGTCCAC TGTGCATAAT ATTTGAGATG TAAAACCATT TTGTGCGGTA TATGTGTTAT
2881 TAGTTGTAAG TCGGTGAAAT GTACATCTGA ATTCTGTGTG CATATTGTTG GTACTGATGC
2941 TATTTTCGTG CATATGTCTA GTGTATATGT TTTAAGGCAA ACTTTCTTTG TGTGTTGGGT
3001 GTGTATGTGA CACGAATGGG GACAGCATCT GTATTTCTGA GCATGGATTG ATGTGTGGTG
3061 TCTGTATGTA TCTTGGAATG GAGGAGGGAG ATTGAAGAAG TCTGGCTGTG AGCAGCAGAA
3121 ATAATTTCCA AAGTTGAGTG ACATGACTCT AAGATGCCCA GTTTCTCGGC CTGGGGTCAG
3181 CCTGGGTGAT AGCTCAGTCT GTCAGAATGA AAGGAAACAC GGTGCTTCCT TGCTCCACCT
3241 TTTCACAGGC CAGACCACAC CTTCTTCATC CTGAACACAA GGATTTCAAG GGCTTTTGTT
3301 ACCTCTTCCT ACGTTTCCTG CCTCTGCTAT CCGAGGCACT GGCCTCCCTA AACCCTGCCC
3361 TCCTGCCTCA ATAGCAAGTC ATGGTATCCT CACCTCTCCC TTCCCTTTTT GGCTTATCTG
3421 **CCAAACATGT ATAAAAGTCC TTGGTTCCCC ATCTCTACTA AAAATACAA**C AATTAGCCGG
3481 GTGTGATGGC GCGTGCCTGT AGTCCCAGCT AGTTGGGAGG CTGAGGCAGG AGAAACGCTT
3541 GAGCCCGCAA GGTGGAGGTT GCAGTGAGCC GAGATCATGC CACTGCACTC CAGCCTGGTG
3601 ACAGAGCAAG ACTCTGTGTC AAAAAAAAAA AAAAAAAAAA AGCCTTGGTT GTAGGGAGTT
3661 TCTCCTAATC CCTCTGGGAA AGCAAGGGTG GAGGGGAAGC CAGTCAATCT CCCTTCTGTT
3721 GCCGCATGGA AACTCCCTTA AGGCAGGAAG CTGAAAAAAC TGTAGCATTC ACCTCATTAT
3781 TCACCTTGTC TCATGTCTCA CTGTCCTTCC ACATGTCTCA TTGTTACTCC ATATTGGATG
3841 GAAGTAGAAG TCCCTTTGGT ATTTTTTAAA GTCTTTGCCA TGTCTAAGTT AATGAGGTTA
3901 ATGGAGGCAG CAGAGATGGC TCCAGGGTTC TGATAGCAAG TGTCAGGCTG CGTGCTCTGT
3961 AGGCACCAGA AACTGTTGTC ACCAGTAATT TTGATGTGGT CTGAGTTAGA ATGGTCTGAT
4021 TTGCCATGAT CTATTTAACA TAGCTTGATT TAGCGTGTCC TGTGTTCTGA ATTTAAAACT
4081 CACAGTTGTG AA**ACTGATCA GTAAAAAATA AGGGGAGACC AACTAAAAAC CATGTTGTTC**
4141 **TA**TTTATAGA TGTAGTTTTT ACTTATTTCA AAATACGAGG TATTTAGTTT TACATTCAAA
4201 TTGTTCTCTA ACTCTCTAAA ATGTTCTCTG ACTATTTTTG CCCTTAAGGG AGAAACCAGA
4261 TGTCATTGGT CTTACGTGGC TGGTGTTGGG GGTGGGGAGG GTTAAAGAAA CCACGTTCTC
4321 TGTCCTCAGC CAGAAGTTCA GTAATCCAAG GCCAGAGAGT GGACGGCAGA GGCACTGTCC
4381 CTGGGGACCT TGGTTATAAG TTATCCAGAC ACAGGGACCA GAGCCTGGGA GACAAAAAAA
4441 GATGTAGCCC TAGGGCTTTG GGAAAAGGAG GATGGACCCA GTGAATTCCA CGCTTAGCAA
4501 GGACCTAAAC AGTGTCCCCC AAATGAGAGA AGGGAGGACA GAAAGAACAC TTCAGGATGG
4561 AAATGGGCTG ACACTTAACC GTGGAGTGTC TCTGCAAACT TCCTTTGCCA TTCTCCTGTT
4621 TGAGTTTGAT AAACCTGAGA AGAGACTTGG ATAAAGACCG TCACGAAGAC TACACTAATG
4681 AGTTTCTTCT AGCTTTTTTC TACTCACTTT CCCTATCTAT CCTTCACATT GGGAGTTGGC
4741 ATGAGGATCC CAGCAGCCCA TCAGGGGAGG ACTCTAGAGA TCCCTTTCCC CATTGCCTCT
4801 CCTCCCCATA CCCCCAGGCA TATCCTCCCA GGGCACGGAA GCTGAGAAGC AGTCCAGAAC
4861 CACAGTGGGC TAGTGAGGGG TACCTGCTGA TGTACCCTTT GGACAGCATT CTGCCCCACC
4921 CTGCAGGAAG AAGCAGAAGG AGGGAGAGGG TG**AGGCAGAG AATAAATAAC CCTGACCAGG**
4981 **GAGGTCCAAG GGAGTAGGCG GAG**Acagaga ggctgtattt cagtgcagcc tgccagacct

Note: The three high score predictions of promoters were bold and underlined. The lower case sequence indicates the beginning part of the transcript of 101P3A11 gene.

Table XXX, beginning at page 214, line 35, has been amended as follows

Table XXX: Promoters and their positions predicted by Neural Network Promoter Prediction computer program (various portions of SEQ ID NO: 2867, respectively, in order of appearance).

Start	End	Score	Promoter Sequence
25	75	0.91	TTTTGCATTTTTAATAGAGGCAGGGTTTCACCATGTTGGCCTGGCTGGTC
665	715	0.95	CAGGAAGTTGTATATAAGGAGAATCAGAGCAGAGAGAGACTAGGGTTCAG
2477	2527	0.91	TCAGTGTGCGTATATGTGAGAGAGAGGGTGCACACATGGAATACGTACTG
3139	3189	0.82	TGACATGACTCTAAGATGCCCAGTTTCTCGGCCTGGGGTCAGCCTGGGTG
3420	3470	0.96	GCCAAACATGTATAAAAGTCCTTGGTTCCCCATCTCTACTAAAAATACAA
4092	4142	0.99	AACTGATCAGTAAAAAATAAGGGGAGACCAACTAAAAACCATGTTGTTCT
4953	5003	0.97	AGGCAGAGAATAAATAACCCTGACCAGGGAGGTCCAAGGGAGTAGGCGGA

Table XXXI, beginning at page 215, line 1, has been amended as follows:

Table XXXI: Alignment of five homologous 5' upstream genomic regulatory regions of the human 101P3A11 and PSA genes.

Query: 5' upstream regulatory region of the PSA gene
Subject: Putative 5' upstream regulatory region of the 101P3A11 gene.
Nucleic acid sequences predicted to be binding sites for the indicated transcription factors are **bolded**, underlined, or *italicized*.

```
1.                    NF-1 SP-1 NF-1
Query: 3864 ccaggctggagtgcagtggcgcagtctcggctcactgcaacctctgcctcccaggttcaa 3923
(SEQ ID NO: 2868)
            ||||||||||||||||||||    ||||||||||||||||||||  |||  | || ||||
Sbjct: 3598 ccaggctggagtgcagtggcatgatctcggctcactgcaacctccaccttgcgggctcaa 3539
(SEQ ID NO: 2869)

Query: 3924 gtgattctcctgcctcagcctcctgagttgctgggattacaggcatgcagcaccatgccc 3983
            | | ||||||||||||||||||||  | | |||||| |||||||| ||  || ||  |||
Sbjct: 3538 gcgtttctcctgcctcagcctcccaactagctgggactacaggcacgcgccatcacaccc 3479

Query: 3984 agctaatttttgtatttttagtagagatgggg 4015
            ||||||| ||||||||||||||||||||||||
Sbjct: 3478 ggctaattgttgtatttttagtagagatgggg 3447


2.
Query: 4670 cctgtaatcccagctactgaggaggctgaggcaggagaatcacttgaacccagaaggcag 4729
(SEQ ID NO: 2870)
            |||||| ||||||||| |  |||||||||||||||||| | ||||| |||  ||||  |
Sbjct: 3496 cctgtagtcccagctagttgggaggctgaggcaggagaaacgcttgagcccgcaaggtgg 3555
(SEQ ID NO: 2871)
                                          SP1                 NF-E
                                  NF-1    NF-1          GR      GR
Query: 4730 aggttgcaatgagccgagattgcgccactgcactccagcctgggtgacagagtgagactc 4789
            |||||||| ||||||||||   |||||||||||||||||| |||||||||  ||||||
Sbjct: 3556 aggttgcagtgagccgagatcatgccactgcactccagcct-ggtgacagagcaagactc 3614

Query: 4790 tgtctcaaaaaaaaaaaa 4807
            ||| |||||||||||||
Sbjct: 3615 tgtgtcaaaaaaaaaaaa 3632
```

3.

```
                          GR            NF-1 SP1
Query: 142  tgagactgagtctcgctctgtgcccaggctggagtgcagtggtgcaaccttggctcactg 201
(SEQ ID NO: 2872)
            ||| || |||||| |||||||  ||||||||||||||||||    | || |||||||||
Sbjct: 3621 tgacacagagtcttgctctgtcaccaggctggagtgcagtggcatgatctcggctcactg 3562
(SEQ ID NO: 2873)

Query: 202  caagctccgcctcctgggttcacgccattctcctgcctcagcctcctgagtagctgggac 261
             ||| |||| |||   ||| ||| ||  ||||||||||||||||||  | ||||||||||
Sbjct: 3561 caacctccaccttgcgggctcaagcgtttctcctgcctcagcctcccaactagctgggac 3502

                       NF-1
Query: 262  tacaggcacccgccaccacgcctggctaannnnnnngtatttttagtagagatgggg 318
             ||||||||| ||||| ||| || ||||||       ||||||||||||||||||||
Sbjct: 3501 tacaggcacgcgccatcacacccggctaa--ttgttgtatttttagtagagatgggg 3447
```

4.

```
Query: 300 atttttagtagagatggggtttcactgtgttagccaggatggtctcagtctcctgacctc 359
(SEQ ID NO: 2874)
           ||||||| |||||   |||||||||  |||| ||| || |||||||   | ||||||||
Sbjct: 31  atttttaatagaggcagggtttcaccatgttggcctggctggtctcgaacccctgacctt 90
(SEQ ID NO: 2875)
                    SP1                                              NF-1
                 LF-A1                                          CP2
Query: 360 gtgatctgcccacctggcctcccaaagtgctgggattacaggcgtgagccactgcgcct 419
           | |||||||||||||| ||||||||||||||||||||||||||||||||||||  |||
Sbjct: 91  gcgatctgcccacctcggcctcccaaagtgctgggattacaggcgtgagccactgtacct 150

          NF-1
Query: 420 ggc 422
           |||
Sbjct: 151 ggc 153
```

5.

```
                          NF-1
              NF-1       CP2
Query: 4506 gccaggcacagtggctcacgcctgtaatcccaacaccatgggaggctgagatgggtggat 4565
(SEQ ID NO: 2876)
             |||||| |||||||||||||||||||||||| |||  |||||||| ||| ||||  |||
Sbjct: 153  gccaggtacagtggctcacgcctgtaatcccagcactttgggaggccgaggtgggcagat 94
(SEQ ID NO: 2877)

Query: 4566 cacgaggtcaggagtttgagaccagcctgaccaacatggtgaaactctgtctcta 4620
            | | |||||||| ||| |||||||||| | ||||||||||||||| ||| |||||
Sbjct: 93   cgcaaggtcaggggttcgagaccagccaggccaacatggtgaaaccctgcctcta 39
```

Figure 1 (SEQ ID NO:2878)

GATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACATTTTGGAAGACAGTATTCAGAAAAAAAAATTTCC
TTAATAAAAATACAACTCAGATCCTTCAAATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTATTTTCTTCTTTGTTTTC
TTGCTACGTATAATTATTAATATCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTTACCATGCAGTCCAAATCTAAAC
TGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACAGCAAAGGAA
AATAAACACAGAATATAATAAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTTTAGAACTCCCAACCACATTTGGATC

FIG. 2A (SEQ ID NOS:2879 & 2880)

```
                9          18          27          36          45          54
5'  CAG AGA GGC TGT ATT TCA GTG CAG CCT GCC AGA CCT CTT CTG GAG GAA GAC TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
               63          72          81          90          99         108
    ACA AAG GGG GTC ACA CAT TCC TTC CAT ACG GTT GAG CCT CTA CCT GCC TGG TGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

              117         126         135         144         153         162
    TGG TCA CAG TTC AGC TTC TTC ATG ATG GTG GAT CCC AAT GGC AAT GAA TCC AGT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
                                    M   M   V   D   P   N   G   N   E   S   S

              171         180         189         198         207         216
    GCT ACA TAC TTC ATC CTA ATA GGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     A   T   Y   F   I   L   I   G   L   P   G   L   E   E   A   Q   F   W

              225         234         243         252         261         270
    TTG GCC TTC CCA TTG TGC TCC CTC TAC CTT ATT GCT GTG CTA GGT AAC TTG ACA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   A   F   P   L   C   S   L   Y   L   I   A   V   L   G   N   L   T

              279         288         297         306         315         324
    ATC ATC TAC ATT GTG CGG ACT GAG CAC AGC CTG CAT GAG CCC ATG TAT ATA TTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     I   I   Y   I   V   R   T   E   H   S   L   H   E   P   M   Y   I   F

              333         342         351         360         369         378
    CTT TGC ATG CTT TCA GGC ATT GAC ATC CTC ATC TCC ACC TCA TCC ATG CCC AAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   C   M   L   S   G   I   D   I   L   I   S   T   S   S   M   P   K

              387         396         405         414         423         432
    ATG CTG GCC ATC TTC TGG TTC AAT TCC ACT ACC ATC CAG TTT GAT GCT TGT CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   L   A   I   F   W   F   N   S   T   T   I   Q   F   D   A   C   L

              441         450         459         468         477         486
    CTA CAG ATT TTT GCC ATC CAC TCC TTA TCT GGC ATG GAA TCC ACA GTG CTG CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   Q   I   F   A   I   H   S   L   S   G   M   E   S   T   V   L   L

              495         504         513         522         531         540
    GCC ATG GCT TTT GAC CGC TAT GTG GCC ATC TGT CAC CCA CTG CGC CAT GCC ACA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     A   M   A   F   D   R   Y   V   A   I   C   H   P   L   R   H   A   T

              549         558         567         576         585         594
    GTA CTT ACG TTG CCT CGT GTC ACC AAA ATT GGT GTG GCT GCT GTG GTG CGG GGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   L   T   L   P   R   V   T   K   I   G   V   A   A   V   V   R   G

              603         612         621         630         639         648
    GCT GCA CTG ATG GCA CCC CTT CCT GTC TTC ATC AAG CAG CTG CCC TTC TGC CGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     A   A   L   M   A   P   L   P   V   F   I   K   Q   L   P   F   C   R
```

FIG. 2B

```
        657         666         675         684         693         702
TCC AAT ATC CTT TCC CAT TCC TAC TGC CTA CAC CAA GAT GTC ATG AAG CTG GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   N   I   L   S   H   S   Y   C   L   H   Q   D   V   M   K   L   A

        711         720         729         738         747         756
TGT GAT GAT ATC CGG GTC AAT GTC GTC TAT GGC CTT ATC GTC ATC ATC TCC GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   D   D   I   R   V   N   V   V   Y   G   L   I   V   I   I   S   A

        765         774         783         792         801         810
ATT GGC CTG GAC TCA CTT CTC ATC TCC TTC TCA TAT CTG CTT ATT CTT AAG ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   G   L   D   S   L   L   I   S   F   S   Y   L   L   I   L   K   T

        819         828         837         846         855         864
GTG TTG GGC TTG ACA CGT GAA GCC CAG GCC AAG GCA TTT GGC ACT TGC GTC TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   L   G   L   T   R   E   A   Q   A   K   A   F   G   T   C   V   S

        873         882         891         900         909         918
CAT GTG TGT GCT GTG TTC ATA TTC TAT GTA CCT TTC ATT GGA TTG TCC ATG GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   V   C   A   V   F   I   F   Y   V   P   F   I   G   L   S   M   V

        927         936         945         954         963         972
CAT CGC TTT AGC AAG CGG CGT GAC TCT CCG CTG CCC GTC ATC TTG GCC AAT ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   R   F   S   K   R   R   D   S   P   L   P   V   I   L   A   N   I

        981         990         999        1008        1017        1026
TAT CTG CTG GTT CCT CCT GTG CTC AAC CCA ATT GTC TAT GGA GTG AAG ACA AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   L   L   V   P   P   V   L   N   P   I   V   Y   G   V   K   T   K

       1035        1044        1053        1062        1071        1080
GAG ATT CGA CAG CGC ATC CTT CGA CTT TTC CAT GTG GCC ACA CAC GCT TCA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   I   R   Q   R   I   L   R   L   F   H   V   A   T   H   A   S   E

       1089        1098        1107        1116        1125        1134
CCC TAG GTG TCA GTG ATC AAA CTT CTT TTC CAT TCA GAG TCC TCT GAT TCA GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   *

       1143        1152        1161        1170        1179        1188
TTT AAT GTT AAC ATT TTG GAA GAC AGT ATT CAG AAA AAA AAT TTC CTT AAT AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1197        1206        1215        1224        1233        1242
AAA TAC AAC TCA GAT CCT TCA AAT ATG AAA CTG GTT GGG GAA TCT CCA TTT TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1251        1260        1269        1278        1287        1296
CAA TAT TAT TTT CTT CTT TGT TTT CTT GCT ACA TAT AAT TAT TAA TAC CCT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1305        1314        1323        1332        1341        1350
TAG GTT GTG GTT GGA GGG TTA TTA CTT TTC ATT TTA CCA TGC AGT CCA AAT CTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
```

FIG. 2C

```
   1359        1368        1377        1386        1395        1404
AAC TGC TTC TAC TGA TGG TTT ACA GCA TTC TGA GAT AAG AAT GGT ACA TCT AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1413        1422        1431        1440        1449        1458
GAA CAT TTG CCA AAG GCC TAA GCA CGG CAA AGG AAA ATA AAC ACA GAA TAT AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1467        1476        1485        1494        1503        1512
AAA ATG AGA TAA TCT AGC TTA AAA CTA TAA CTT CCT CTT CAG AAC TCC CAA CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1521        1530        1539        1548        1557        1566
CAT TGG ATC TCA GAA AAA TGC TGT CTT CAA AAT GAC TTC TAC AGA GAA GAA ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1575        1584        1593        1602        1611        1620
ATT TTT CCT CTG GAC ACT AGC ACT TAA GGG GAA GAT TGG AAG TAA AGC CTT GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1629        1638        1647        1656        1665        1674
AAG AGT ACA TTT ACC TAC GTT AAT GAA AGT TGA CAC ACT GTT CTG AGA GTT TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1683        1692        1701        1710        1719        1728
ACA GCA TAT GGA CCC TGT TTT TCC TAT TTA ATT TTC TTA TCA ACC CTT TAA TTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1737        1746        1755        1764        1773        1782
GGC AAA GAT ATT ATT AGT ACC CTC ATT GTA GCC ATG GGA AAA TTG ATG TTC AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1791        1800        1809        1818        1827        1836
GGG GAT CAG TGA ATT AAA TGG GGT CAT ACA AGT ATA AAA ATT AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1845        1854        1863        1872        1881        1890
GAC TTC ATG CCC AAT CTC ATA TGA TGT GGA AGA ACT GTT AGA GAG ACC AAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1899        1908        1917        1926        1935        1944
GTA GTG GGT TAG AGA TTT CCA GAG TCT TAC ATT TTC TAG AGG AGG TAT TTA ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1953        1962        1971        1980        1989        1998
TCT TCT CAC TCA TCC AGT GTT GTA TTT AGG AAT TTC CTG GCA ACA GAA CTC ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2007        2016        2025        2034        2043        2052
GCT TTA ATC CCA CTA GCT ATT GCT TAT TGT CCT GGT CCA ATT GCC AAT TAC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2061        2070        2079        2088        2097        2106
TGT CTT GGA AGA AGT GAT TTC TAG GTT CAC CAT TAT GGA AGA TTC TTA TTC AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2115        2124        2133        2142        2151        2160
AAG TCT GCA TAG GGC TTA TAG CAA GTT ATT TAT TTT TAA AAG TTC CAT AGG TGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2169        2178        2187        2196        2205        2214
TTC TGA TAG GCA GTG AGG TTA GGG AGC CAC CAG TTA TGA TGG GAA GTA TGG AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2223        2232        2241        2250        2259        2268
GGC AGG TCT TGA AGA TAA CAT TGG CCT TTT GAG TGT GAC TCG TAG CTG GAA AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2277        2286        2295        2304        2313        2322
GAG GGA ATC TTC AGG ACC ATG CTT TAT TTG GGG CTT TGT GCA GTA TGG AAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2331        2340        2349        2358        2367        2376
GAC TTT GAG ACC AGG AAA GCA ATC TGA CTT AGG CAT GGG AAT CAG GCA TTT TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
```

10091469.050802

FIG. 2D

```
     2385        2394        2403        2412        2421        2430
CTT CTG AGG GGC TAT TAC CAA GGG TTA ATA GGT TTC ATC TTC AAC AGG ATA TGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2439        2448        2457        2466        2475        2484
CAA CAG TGT TAA CCA AGA AAC TCA AAT TAC AAA TAC TAA AAC ATG TGA TCA TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2493        2502        2511        2520        2529        2538
ATG TGG TAA GTT TCA TTT TCT TTT TCA ATC CTC AGG TTC CCT GAT ATG GAT TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2547        2556        2565        2574        2583        2592
TAT AAC ATG CTT TCA TCC CCT TTT GTA ATG GAT ATC ATA TTT GGA AAT GCC TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2601        2610        2619        2628        2637        2646
TTA ATA CTT GTA TTT GCT GCT GGA CTG TAA GCC CAT GAG GGC ACT GTT TAT TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2655        2664        2673        2682        2691        2700
TGA ATG TCA TCT CTG TTC ATC ATT GAC TGC TCT TTG CTC ATC ATT GAA TCC CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2709        2718        2727        2736        2745        2754
AGC AAA GTG CCT AGA ACA TAA TAG TGC TTA TGC TTG ACA CCG GTT ATT TTT CAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2763        2772        2781        2790        2799        2808
CAA ACC TGA TTC CTT CTG TCC TGA ACA CAT AGC CAG GCA ATT TTC CAG CCT TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2817        2826        2835        2844        2853        2862
TTG AGT TGG GTA TTA TTA AAT TCT GGC CAT TAC TTC CAA TGT GAG TGG AAG TGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2871        2880        2889        2898        2907        2916
CAT GTG CAA TTT CTA TAC CTG GCT CAT AAA ACC CTC CCA TGT GCA GCC TTT CAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2925        2934        2943        2952        2961        2970
GTT GAC ATT AAA TGT GAC TTG GGA AGC TAT GTG TTA CAC AGA GTA AAT CAC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2979        2988        2997        3006        3015        3024
AAG CCT GGA TTT CTG AAA AAA CTG TGC AGA GCC AAA CCT CTG TCA TTT GCA ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       3033        3042        3051        3060        3069        3078
CCC ACT TGT ATT TGT ACG AGG CAG TTG GAT AAG TGA AAA ATA AAG TAC TAT TGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       3087        3096        3105        3114        3123        3132
GTC AAG AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

AAA A 3'
--- -
```

Figure 3: Protein Sequence for 101P3A11 **(piece of SEQ ID NO:2880)**

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILI
STSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPRVTKIGV
AAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYL
LILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYG
VKTKEIRQRILRLFHVATHASEP

10001469 .052002

Figure 4

Alignment of 101P3A11 (Sbjct) with mouse olfactory receptor S25 (Query)

```
Query: 34  GNYTVVTEFILLGLTDDITVSVILFVMFLIVYSVTLMGNLNIIVLIRTSPQLHTPMYLFL 93
           GN +  T FIL+GL          L      +Y + ++GNL II ++RT   LH PMY+FL
Sbjct: 6   GNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL 65

Query: 94  SHLAFLDIGYSSSVTPIMLRGFLRKGTFIPVAGCVAQLCIVVAFGTSESFLLASMAYDRY 153
             L+ +DI  S+S  P ML  F    T I    C+ Q+  + +    ES +L +MA+DRY
Sbjct: 66  CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRY 125

Query: 154 VAICSPLLYSTQMSSTVCILLVGTSYLGGWVNAWIFTGCSLNLSFCGPNKINHFFCDYSP 213
           VAIC PL ++T ++      +   + + G             L FC  N ++H +C +
Sbjct: 126 VAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQD 185

Query: 214 LLKLSCSHDFSFEVIPAISSGSIIVVTVFIIALSYVYILVSILKMRSTEGRQKAFSTCTS 273
           ++KL+C       V   I   S I +   +I+ SY+ IL ++L + + E + KAF TC S
Sbjct: 186 VMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244

Query: 274 HLTAVTLFFGTITFIYVMPQSSYSTDQNK----VVSVFYTVVIPMLNPLIYSFRNKEVKE 329
           H+ AV +F+  + FI +     +S  ++      +++  Y +V P+LNP++Y  + KE+++
Sbjct: 245 HVCAVFIFY--VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQ 302

Query: 330 AMKKL 334 (SEQ ID NO:2881)
             + +L
Sbjct: 303 RILRL 307 (SEQ ID NO:2882)
```

10001469.052202

Figure 23: Alignment of 101P3A11-PHOR-1 with the rat GPCR RA1C (gi|3420759).

Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%)

```
PHOR: 14  FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
          F+LIG+PGLEEA FW  FPL S+Y +A+ GN  +++IVRTE SLH PMY+FLCML+ ID+
RA1C: 11  FMLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70

PHOR: 74  LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
            +STS+MPK+LA+FWF+S  I FDACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
RA1C: 71  ALSTSTMPKILALFWFDSREITFDACLAQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134 HATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
           HA VL       +IG+ A+VRG+     PLP+ IK+L FC SN+LSHSYC+HQDVMKLA  D
RA1C: 131 HAAVLNNTVTVQIGMVALVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYTD 190

PHOR: 194 IRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
              NVVYGL  I+  +G+D + IS SY LI++ VL L ++  +AKAFGTCVSH+  V  F
RA1C: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSHIGVVLAF 250

PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311 (SEQ ID NO:2883)
           YVP IGLS+VHRF     D  + V++ ++YLL+PPV+NPI+YG KTK+IR R+L +F ++
RA1C: 251 YVPLIGLSVVHRFGNSLDPIVHVLMGDVYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO:2884)
```

10001469.052002

Figure 24: Alignment of 101P3A11-PHOR-1 with the human prostate specific GPCR. (gi|13540539)

Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%)

```
PHOR: 14   FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
           F+LIG+PGLE+A FW+ FPL S+Y++A+ GN  +++IVRTE SLH PMY+FLCML+ ID+
GPCR: 11   FVLIGIPGLEKAHFWVGFPLLSMYVVAMFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70

PHOR: 74   LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
            +STS+MPK+LA+FWF+S  I F+ACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
GPCR: 71   ALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134  HATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
           HA VL       +IG+ AVVRG+     PLP+ IK+L FC SN+LSHSYC+HQDVMKLA D
GPCR: 131  HAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYAD 190

PHOR: 194  IRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
              NVVYGL  I+  +G+D + IS SY LI++TVL L ++  +AKAFGTCVSH+  V  F
GPCR: 191  TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAF 250

PHOR: 253  YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311 (SEQ ID NO:2885)
           YVP IGLS+VHRF       + V++ +IYLL+PPV+NPI+YG KTK+IR R+L +F ++
GPCR: 251  YVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO:2886)
```

Figure 25: Alignment with human olfactory receptor 5II12 (gi|14423836)

```
Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%)

PHOR: 7   NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLC 66
          N +   +F+L G+PGLE +  WL+ PLC +Y +A+ GN  I+  VR E SLHEPMY FL
HOR5: 5   NVTHPAFFLLTGIPGLESSHSWLSGPLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFLS 64

PHOR: 67  MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126
          MLS  D+ IS +++P +L  F  N+  I FDACL+Q+F IH  S MES +LLAM+FDRYV
HOR5: 65  MLSFSDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYV 124

PHOR: 127 AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186
          AIC PLR+ATVLT   +  +G+ A  R    + PLP  IK+LP CRSN+LSHSYCLH D+
HOR5: 125 AICDPLRYATVLTTEVIAAMGLGAAARSFITLFPLPFLIKRLPICRSNVLSHSYCLHPDM 184

PHOR: 187 MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245
          M+LAC DI +N +YGL V++S  G+D   I  SY+LIL++V+   +RE + KA  TCVSH
HOR5: 185 MRLACADISINSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSH 244

PHOR: 246 VCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRIL 305
          + AV  FYVP IG+S VHRF K      + V+++N+YL VPPVLNP++Y  KTKEIR+ I
HOR5: 245 ILAVLAFYVPMIGVSTVHRFGKHVPCYIHVLMSNVYLFVPPVLNPLIYSAKTKEIRRAIF 304

PHOR: 306 RLFH 309  (SEQ ID NO:2887)
          R+FH
HOR5: 305 RMFH 308  (SEQ ID NO:2888)
```

Figure 1 (SEQ ID NO: 2878)

GATCAAACTTCTTTTCCATTCAGAGTCCTCTGATTCAGATTTTAATGTTAACATTTTGGAAGACAGTATTCAGAAAAAAAAATTTCC
TTAATAAAAATACAACTCAGATCCTTCAAATATGAAACTGGTTGGGGAATCTCCATTTTTTCAATATTATTTTCTTCTTTGTTTTC
TTGCTACGTATAATTATTAATATCCTGACTAGGTTGTGGTTGGAGGGTTATTACTTTTCATTTTACCATGCAGTCCAAATCTAAAC
TGCTTCTACTGATGGTTTACAGCATTCTGAGATAAGAATGGTACATCTAGAGAACATTTGCCAAAGGCCTAAGCACAGCAAAGGAA
AATAAACACAGAATATAATAAAATGAGATAATCTAGCTTAAAACTATAACTTCCTCTTTAGAACTCCCAACCACATTTGGATC

FIG. 2A (SEQ ID NOS: 2879 & 2880)

```
                9          18          27          36          45          54
5'  CAG AGA GGC TGT ATT TCA GTG CAG CCT GCC AGA CCT CTT CTG GAG GAA GAC TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
               63          72          81          90          99         108
    ACA AAG GGG GTC ACA CAT TCC TTC CAT ACG GTT GAG CCT CTA CCT GCC TGG TGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

              117         126         135         144         153         162
    TGG TCA CAG TTC AGC TTC TTC ATG ATG GTG GAT CCC AAT GGC AAT GAA TCC AGT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
                                    M   M   V   D   P   N   G   N   E   S   S

              171         180         189         198         207         216
    GCT ACA TAC TTC ATC CTA ATA GGC CTC CCT GGT TTA GAA GAG GCT CAG TTC TGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     A   T   Y   F   I   L   I   G   L   P   G   L   E   E   A   Q   F   W

              225         234         243         252         261         270
    TTG GCC TTC CCA TTG TGC TCC CTC TAC CTT ATT GCT GTG CTA GGT AAC TTG ACA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   A   F   P   L   C   S   L   Y   L   I   A   V   L   G   N   L   T

              279         288         297         306         315         324
    ATC ATC TAC ATT GTG CGG ACT GAG CAC AGC CTG CAT GAG CCC ATG TAT ATA TTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     I   I   Y   I   V   R   T   E   H   S   L   H   E   P   M   Y   I   F

              333         342         351         360         369         378
    CTT TGC ATG CTT TCA GGC ATT GAC ATC CTC ATC TCC ACC TCA TCC ATG CCC AAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   C   M   L   S   G   I   D   I   L   I   S   T   S   S   M   P   K

              387         396         405         414         423         432
    ATG CTG GCC ATC TTC TGG TTC AAT TCC ACT ACC ATC CAG TTT GAT GCT TGT CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     M   L   A   I   F   W   F   N   S   T   T   I   Q   F   D   A   C   L

              441         450         459         468         477         486
    CTA CAG ATT TTT GCC ATC CAC TCC TTA TCT GGC ATG GAA TCC ACA GTG CTG CTG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     L   Q   I   F   A   I   H   S   L   S   G   M   E   S   T   V   L   L

              495         504         513         522         531         540
    GCC ATG GCT TTT GAC CGC TAT GTG GCC ATC TGT CAC CCA CTG CGC CAT GCC ACA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     A   M   A   F   D   R   Y   V   A   I   C   H   P   L   R   H   A   T

              549         558         567         576         585         594
    GTA CTT ACG TTG CCT CGT GTC ACC AAA ATT GGT GTG GCT GCT GTG GTG CGG GGG
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     V   L   T   L   P   R   V   T   K   I   G   V   A   A   V   V   R   G

              603         612         621         630         639         648
    GCT GCA CTG ATG GCA CCC CTT CCT GTC TTC ATC AAG CAG CTG CCC TTC TGC CGC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
     A   A   L   M   A   P   L   P   V   F   I   K   Q   L   P   F   C   R
```

FIG. 2B

```
        657         666         675         684         693         702
TCC AAT ATC CTT TCC CAT TCC TAC TGC CTA CAC CAA GAT GTC ATG AAG CTG GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 S   N   I   L   S   H   S   Y   C   L   H   Q   D   V   M   K   L   A

        711         720         729         738         747         756
TGT GAT GAT ATC CGG GTC AAT GTC GTC TAT GGC CTT ATC GTC ATC ATC TCC GCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 C   D   D   I   R   V   N   V   V   Y   G   L   I   V   I   I   S   A

        765         774         783         792         801         810
ATT GGC CTG GAC TCA CTT CTC ATC TCC TTC TCA TAT CTG CTT ATT CTT AAG ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 I   G   L   D   S   L   L   I   S   F   S   Y   L   L   I   L   K   T

        819         828         837         846         855         864
GTG TTG GGC TTG ACA CGT GAA GCC CAG GCC AAG GCA TTT GGC ACT TGC GTC TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 V   L   G   L   T   R   E   A   Q   A   K   A   F   G   T   C   V   S

        873         882         891         900         909         918
CAT GTG TGT GCT GTG TTC ATA TTC TAT GTA CCT TTC ATT GGA TTG TCC ATG GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   V   C   A   V   F   I   F   Y   V   P   F   I   G   L   S   M   V

        927         936         945         954         963         972
CAT CGC TTT AGC AAG CGG CGT GAC TCT CCG CTG CCC GTC ATC TTG GCC AAT ATC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 H   R   F   S   K   R   R   D   S   P   L   P   V   I   L   A   N   I

        981         990         999        1008        1017        1026
TAT CTG CTG GTT CCT CCT GTG CTC AAC CCA ATT GTC TAT GGA GTG AAG ACA AAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 Y   L   L   V   P   P   V   L   N   P   I   V   Y   G   V   K   T   K

       1035        1044        1053        1062        1071        1080
GAG ATT CGA CAG CGC ATC CTT CGA CTT TTC CAT GTG GCC ACA CAC GCT TCA GAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 E   I   R   Q   R   I   L   R   L   F   H   V   A   T   H   A   S   E

       1089        1098        1107        1116        1125        1134
CCC TAG GTG TCA GTG ATC AAA CTT CTT TTC CAT TCA GAG TCC TCT GAT TCA GAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
 P   *

       1143        1152        1161        1170        1179        1188
TTT AAT GTT AAC ATT TTG GAA GAC AGT ATT CAG AAA AAA AAT TTC CTT AAT AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1197        1206        1215        1224        1233        1242
AAA TAC AAC TCA GAT CCT TCA AAT ATG AAA CTG GTT GGG GAA TCT CCA TTT TTT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1251        1260        1269        1278        1287        1296
CAA TAT TAT TTT CTT CTT TGT TTT CTT GCT ACA TAT AAT TAT TAA TAC CCT GAC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1305        1314        1323        1332        1341        1350
TAG GTT GTG GTT GGA GGG TTA TTA CTT TTC ATT TTA CCA TGC AGT CCA AAT CTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
```

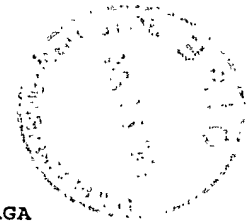


FIG. 2C

```
    1359        1368        1377        1386        1395        1404
AAC TGC TTC TAC TGA TGG TTT ACA GCA TTC TGA GAT AAG AAT GGT ACA TCT AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1413        1422        1431        1440        1449        1458
GAA CAT TTG CCA AAG GCC TAA GCA CGG CAA AGG AAA ATA AAC ACA GAA TAT AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1467        1476        1485        1494        1503        1512
AAA ATG AGA TAA TCT AGC TTA AAA CTA TAA CTT CCT CTT CAG AAC TCC CAA CCA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1521        1530        1539        1548        1557        1566
CAT TGG ATC TCA GAA AAA TGC TGT CTT CAA AAT GAC TTC TAC AGA GAA GAA ATA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1575        1584        1593        1602        1611        1620
ATT TTT CCT CTG GAC ACT AGC ACT TAA GGG GAA GAT TGG AAG TAA AGC CTT GAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1629        1638        1647        1656        1665        1674
AAG AGT ACA TTT ACC TAC GTT AAT GAA AGT TGA CAC ACT GTT CTG AGA GTT TTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1683        1692        1701        1710        1719        1728
ACA GCA TAT GGA CCC TGT TTT TCC TAT TTA ATT TTC TTA TCA ACC CTT TAA TTA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1737        1746        1755        1764        1773        1782
GGC AAA GAT ATT ATT AGT ACC CTC ATT GTA GCC ATG GGA AAA TTG ATG TTC AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1791        1800        1809        1818        1827        1836
GGG GAT CAG TGA ATT AAA TGG GGT CAT ACA AGT ATA AAA ATT AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1845        1854        1863        1872        1881        1890
GAC TTC ATG CCC AAT CTC ATA TGA TGT GGA AGA ACT GTT AGA GAG ACC AAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1899        1908        1917        1926        1935        1944
GTA GTG GGT TAG AGA TTT CCA GAG TCT TAC ATT TTC TAG AGG AGG TAT TTA ATT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       1953        1962        1971        1980        1989        1998
TCT TCT CAC TCA TCC AGT GTT GTA TTT AGG AAT TTC CTG GCA ACA GAA CTC ATG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2007        2016        2025        2034        2043        2052
GCT TTA ATC CCA CTA GCT ATT GCT TAT TGT CCT GGT CCA ATT GCC AAT TAC CTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2061        2070        2079        2088        2097        2106
TGT CTT GGA AGA AGT GAT TTC TAG GTT CAC CAT TAT GGA AGA TTC TTA TTC AGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2115        2124        2133        2142        2151        2160
AAG TCT GCA TAG GGC TTA TAG CAA GTT ATT TAT TTT TAA AAG TTC CAT AGG TGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2169        2178        2187        2196        2205        2214
TTC TGA TAG GCA GTG AGG TTA GGG AGC CAC CAG TTA TGA TGG GAA GTA TGG AAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2223        2232        2241        2250        2259        2268
GGC AGG TCT TGA AGA TAA CAT TGG CCT TTT GAG TGT GAC TCG TAG CTG GAA AGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2277        2286        2295        2304        2313        2322
GAG GGA ATC TTC AGG ACC ATG CTT TAT TTG GGG CTT TGT GCA GTA TGG AAC AGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2331        2340        2349        2358        2367        2376
GAC TTT GAG ACC AGG AAA GCA ATC TGA CTT AGG CAT GGG AAT CAG GCA TTT TTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
```

FIG. 2D

```
     2385        2394        2403        2412        2421        2430
CTT CTG AGG GGC TAT TAC CAA GGG TTA ATA GGT TTC ATC TTC AAC AGG ATA TGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2439        2448        2457        2466        2475        2484
CAA CAG TGT TAA CCA AGA AAC TCA AAT TAC AAA TAC TAA AAC ATG TGA TCA TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2493        2502        2511        2520        2529        2538
ATG TGG TAA GTT TCA TTT TCT TTT TCA ATC CTC AGG TTC CCT GAT ATG GAT TCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2547        2556        2565        2574        2583        2592
TAT AAC ATG CTT TCA TCC CCT TTT GTA ATG GAT ATC ATA TTT GGA AAT GCC TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2601        2610        2619        2628        2637        2646
TTA ATA CTT GTA TTT GCT GCT GGA CTG TAA GCC CAT GAG GGC ACT GTT TAT TAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2655        2664        2673        2682        2691        2700
TGA ATG TCA TCT CTG TTC ATC ATT GAC TGC TCT TTG CTC ATC ATT GAA TCC CCC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2709        2718        2727        2736        2745        2754
AGC AAA GTG CCT AGA ACA TAA TAG TGC TTA TGC TTG ACA CCG GTT ATT TTT CAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2763        2772        2781        2790        2799        2808
CAA ACC TGA TTC CTT CTG TCC TGA ACA CAT AGC CAG GCA ATT TTC CAG CCT TCT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2817        2826        2835        2844        2853        2862
TTG AGT TGG GTA TTA TTA AAT TCT GGC CAT TAC TTC CAA TGT GAG TGG AAG TGA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2871        2880        2889        2898        2907        2916
CAT GTG CAA TTT CTA TAC CTG GCT CAT AAA ACC CTC CCA TGT GCA GCC TTT CAT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2925        2934        2943        2952        2961        2970
GTT GAC ATT AAA TGT GAC TTG GGA AGC TAT GTG TTA CAC AGA GTA AAT CAC CAG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       2979        2988        2997        3006        3015        3024
AAG CCT GGA TTT CTG AAA AAA CTG TGC AGA GCC AAA CCT CTG TCA TTT GCA ACT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       3033        3042        3051        3060        3069        3078
CCC ACT TGT ATT TGT ACG AGG CAG TTG GAT AAG TGA AAA ATA AAG TAC TAT TGT
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
       3087        3096        3105        3114        3123        3132
GTC AAG AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA AAA
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---

AAA A 3'
--- -
```

10001469.052002

Figure 3: Protein Sequence for 101P3A11 (piece of SEQ ID NO: 2880)

MVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDILI
STSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLRHATVLTLPRVTKIGV
AAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYL
LILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYG
VKTKEIRQRILRLFHVATHASEP

10001469 .052002

Figure 4

Alignment of 101P3A11 (Sbjct) with mouse olfactory receptor S25 (Query)

```
Query: 34  GNYTVVTEFILLGLTDDITVSVILFVMFLIVYSVTLMGNLNIIVLIRTSPQLHTPMYLFL 93
           GN +  T FIL+GL          L      +Y + ++GNL II ++RT   LH PMY+FL
Sbjct: 6   GNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL 65

Query: 94  SHLAFLDIGYSSSVTPIMLRGFLRKGTFIPVAGCVAQLCIVVAFGTSESFLLASMAYDRY 153
             L+ +DI  S+S  P ML  F    T I    C+ Q+  + +    ES +L +MA+DRY
Sbjct: 66  CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRY 125

Query: 154 VAICSPLLYSTQMSSTVCILLVGTSYLGGWVNAWIFTGCSLNLSFCGPNKINHFFCDYSP 213
           VAIC PL ++T ++       +   + + G              L FC  N ++H +C +
Sbjct: 126 VAICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQD 185

Query: 214 LLKLSCSHDFSFEVIPAISSGSIIVVTVFIIALSYVYILVSILKMRSTEGRQKAFSTCTS 273
           ++KL+C       V   I   S I +   +I+ SY+ IL ++L + + E + KAF TC S
Sbjct: 186 VMKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVS 244

Query: 274 HLTAVTLFFGTITFIYVMPQSSYSTDQNK----VVSVFYTVVIPMLNPLIYSFRNKEVKE 329
           H+ AV +F+  + FI +     +S  ++      +++  Y +V P+LNP++Y  + KE++
Sbjct: 245 HVCAVFIFY--VPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQ 302

Query: 330 AMKKL 334  (SEQ ID NO: 2881)
             + +L
Sbjct: 303 RILRL 307  (SEQ ID NO: 2882)
```

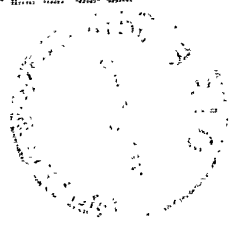


Figure 23: Alignment of 101P3A11-PHOR-1 with the rat GPCR RA1C (gi|3420759).

Identities = 179/299 (59%), Positives = 231/299 (76%), Gaps = 1/299 (0%)

```
PHOR: 14   FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
           F+LIG+PGLEEA FW  FPL S+Y +A+ GN  +++IVRTE SLH PMY+FLCML+ ID+
RA1C: 11   FMLIGIPGLEEAHFWFGFPLLSMYAVALFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70

PHOR: 74   LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
             +STS+MPK+LA+FWF+S  I FDACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
RA1C: 71   ALSTSTMPKILALFWFDSREITFDACLAQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

PHOR: 134  HATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
            HA VL       +IG+ A+VRG+     PLP+ IK+L FC SN+LSHSYC+HQDVMKLA  D
RA1C: 131  HAAVLNNTVTVQIGMVALVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYTD 190

PHOR: 194  IRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
               NVVYGL  I+  +G+D + IS SY LI++ VL L ++  +AKAFGTCVSH+  V  F
RA1C: 191  TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRAVLQLPSKSERAKAFGTCVSHIGVVLAF 250

PHOR: 253  YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311 (SEQ ID NO: 2883)
            YVP IGLS+VHRF    D  + V++ ++YLL+PPV+NPI+YG KTK+IR R+L +F ++
RA1C: 251  YVPLIGLSVVHRFGNSLDPIVHVLMGDVYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO: 2884)
```

[redacted]

Figure 24: Alignment of 101P3A11-PHOR-1 with the human prostate specific GPCR. (gi|13540539)

Identities = 179/299 (59%), Positives = 233/299 (77%), Gaps = 1/299 (0%)

```
PHOR: 14  FILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLCMLSGIDI 73
          F+LIG+PGLE+A FW+ FPL S+Y++A+ GN  +++IVRTE SLH PMY+FLCML+ ID+
GPCR: 11  FVLIGIPGLEKAHFWVGFPLLSMYVVAMFGNCIVVFIVRTERSLHAPMYLFLCMLAAIDL 70

PHOR: 74  LISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYVAICHPLR 133
           +STS+MPK+LA+FWF+S  I F+ACL Q+F IH+LS +EST+LLAMAFDRYVAICHPLR
GPCR: 71  ALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPLR 130

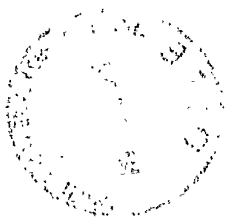
PHOR: 134 HATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDD 193
          HA VL       +IG+ AVVRG+     PLP+ IK+L FC SN+LSHSYC+HQDVMKLA  D
GPCR: 131 HAAVLNNTVTAQIGIVAVVRGSLFFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYAD 190

PHOR: 194 IRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSHVCAVFIF 252
             NVVYGL  I+  +G+D + IS SY LI++TVL L ++  +AKAFGTCVSH+  V  F
GPCR: 191 TLPNVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAF 250

PHOR: 253 YVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRILRLFHVA 311 (SEQ ID NO:2885)
          YVP IGLS+VHRF       + V++ +IYLL+PPV+NPI+YG KTK+IR R+L +F ++
GPCR: 251 YVPLIGLSVVHRFGNSLHPIVRVVMGDIYLLLPPVINPIIYGAKTKQIRTRVLAMFKIS 309 (SEQ ID NO:2886)
```

[redacted]

Figure 25: Alignment with human olfactory receptor 5II12 (gi|14423836)



```
Identities = 163/304 (53%), Positives = 214/304 (69%), Gaps = 1/304 (0%)

PHOR: 7   NESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFLC 66
          N +   +F+L G+PGLE +  WL+ PLC +Y +A+ GN  I+  VR E SLHEPMY FL
HOR5: 5   NVTHPAFFLLTGIPGLESSHSWLSGPLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFLS 64

PHOR: 67  MLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQIFAIHSLSGMESTVLLAMAFDRYV 126
          MLS  D+ IS +++P +L  F  N+  I FDACL+Q+F IH  S MES +LLAM+FDRYV
HOR5: 65  MLSFSDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYV 124

PHOR: 127 AICHPLRHATVLTLPRVTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDV 186
          AIC PLR+ATVLT   +  +G+ A  R    + PLP  IK+LP CRSN+LSHSYCLH D+
HOR5: 125 AICDPLRYATVLTTEVIAAMGLGAAARSFITLFPLPFLIKRLPICRSNVLSHSYCLHPDM 184

PHOR: 187 MKLACDDIRVNVVYGLIVIISAIGLDSLLISFSYLLILKTVLGL-TREAQAKAFGTCVSH 245
          M+LAC DI +N +YGL V++S  G+D   I  SY+LIL++V+   +RE + KA  TCVSH
HOR5: 185 MRLACADISINSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSH 244

PHOR: 246 VCAVFIFYVPFIGLSMVHRFSKRRDSPLPVILANIYLLVPPVLNPIVYGVKTKEIRQRIL 305
          + AV  FYVP IG+S VHRF K      + V+++N+YL VPPVLNP++Y  KTKEIR+ I
HOR5: 245 ILAVLAFYVPMIGVSTVHRFGKHVPCYIHVLMSNVYLFVPPVLNPLIYSAKTKEIRRAIF 304

PHOR: 306 RLFH 309  (SEQ ID NO: 2887)
          R+FH
HOR5: 305 RMFH 308  (SEQ ID NO: 2888)
```